

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 17:11:45 ; Search time 147.679 Seconds
(without alignments)

3569.936 Million cell updates/sec

Title: US-09-373-658C-2

Perfect score: 5189
Sequence: 1 MGNARAPGSRSGFVPVTL.....CDPLKKPKHFIDFCTMAECS 950

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGNPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5189	100.0	4576	4	US-09-130-491-1
2	5176	99.7	4858	4	US-09-392-184-1
3	5174	99.7	3889	4	US-09-568-559-1
4	4287	82.6	3706	4	US-09-484-970B-58
5	3947	76.1	2184	4	US-09-445-023A-2
6	3677	70.9	2184	4	US-09-445-023A-13
7	2284.5	44.0	3638	4	US-09-369-364A-8
8	2176.5	41.9	3126	4	US-09-392-184-7
9	2168	41.8	4192	4	US-09-122-126B-1
10	2168	41.8	4192	4	US-09-634-286A-1
11	1931	37.2	3250	4	US-09-122-126B-14
12	1931	37.2	3250	4	US-09-634-286A-14

13	1918	37.0	3002	4	US-09-369-364A-1	Sequence 1, Appl
14	1756.5	33.9	5804	4	US-09-369-364A-12	Sequence 12, Appl
15	1611	31.0	2625	4	US-09-369-364A-14	Sequence 14, Appl
16	1405.5	27.1	2114	4	US-09-130-491-7	Sequence 7, Appl
17	1320.5	25.4	5357	4	US-09-392-184-5	Sequence 5, Appl
18	1296.5	25.0	3675	4	US-09-930-872-3	Sequence 3, Appl
19	1296.5	25.0	4042	4	US-09-930-872-5	Sequence 5, Appl
20	1213.5	23.4	2727	4	US-09-963-791-1	Sequence 1, Appl
21	1210.5	23.3	3218	4	US-09-369-364A-6	Sequence 6, Appl
22	1198	23.1	3885	4	US-09-369-364A-16	Sequence 16, Appl
23	1152.5	22.2	2274	4	US-09-963-791-23	Sequence 23, Appl
24	1134	21.9	6592	4	US-09-491-522-1	Sequence 1, Appl
25	1118	21.5	4580	4	US-09-491-522-8	Sequence 8, Appl
26	1065.5	20.5	3160	4	US-09-963-791-25	Sequence 25, Appl
27	1041.5	20.1	1520	4	US-09-369-364A-3	Sequence 3, Appl
28	1037.5	20.0	2848	4	US-09-369-364A-4	Sequence 4, Appl
29	966.5	18.6	2450	4	US-09-491-522-2	Sequence 2, Appl
30	965.5	18.6	2450	4	US-09-491-522-9	Sequence 9, Appl
31	780	15.0	1770	4	US-09-963-791-11	Sequence 11, Appl
32	719	13.9	1317	4	US-09-963-791-21	Sequence 21, Appl
33	716.5	13.8	739	4	US-09-369-364A-10	Sequence 10, Appl
34	641	12.4	1810	4	US-09-833-381-1056	Sequence 1056, Ap
35	612.5	11.8	703	4	US-09-392-184-6	Sequence 6, Appl
36	601	11.6	5720	4	US-09-800-729-18	Sequence 18, Appl
37	592.5	11.4	1524	4	US-09-963-791-9	Sequence 9, Appl
38	574.5	11.1	1803	4	US-09-369-364A-20	Sequence 20, Appl
39	531.5	10.2	1071	4	US-09-963-791-19	Sequence 19, Appl
40	508	9.8	2023	4	US-09-491-522-6	Sequence 6, Appl
41	498	9.6	1407	4	US-09-963-791-5	Sequence 5, Appl
42	486	9.4	1476	4	US-09-930-872-1	Sequence 1, Appl
43	440	8.5	852	4	US-09-800-729-54	Sequence 54, Appl
44	438	8.4	3559	4	US-09-800-729-53	Sequence 53, Appl
45	437	8.4	954	4	US-09-963-791-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-130-491-1
; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09130,491
; CURRENT FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)....(3360)

US-09-130-491-1

Alignment Scores:

Pred. No.: 0
Score: 5189.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 4676
Matches: 950
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-373-658C-2 (1-950) x US-09-130-491-1 (1-4676)

no biotech data or for TANGO
no bio tech data or for TANGO
not correct invention, or for TANGO
60/054, 966

QY	1	MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu	20		1591	GTGTGTGATCCGAGCAGAGCTGCTCGTCATAGAGATGATGTTTCAAGAGCTGCCTTC	1650
DB	511	ATGGGGAAACCGCGAGCGGCTCCGGGCTCTCGAGCTTGGGCCCTTACCCACGCTGCTG	570				
QY	21	LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp	40		381	ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaIysGlnCys	400
DB	571	CTGCTCGCGCGCGCTACTGCGCGTGTGCGACGCACTCGGGCGCCCTCCGAGGAGAC	630		1651	ACCACAGCCCATGAATTAGGCCACGTTTAAACATGCCACATGATGCAAAAGCAGTGT	1710
QY	41	GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg	60		401	AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu	420
DB	631	GAGGAGCTAGTGGTCCGAGCTGAGCGCGCCCGGACACGGGACACGCGCTCCGC	690		1711	GCCAGCCTTAATGTGTGAACACAGATTCCACATGATGGCGTCAATGCTTTTCCAACCTG	1770
QY	61	LeuHisAlaPheAspGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla	80		421	AspHisSerGlnProTrpSerProCysSerAlaIleThrMetIleThrSerPheLeuAspAsn	440
DB	691	CTGCACGCTTTTGACACAGCAGCTGATCTGGAGCTGCGCGCCGACAGCAGCTTTTGGCG	750		1771	GACCACAGCAGCAGCTGCTGCTCTTCAGTGCCTACATGATTACATCATTTCTGGATAAT	1830
QY	81	ProGlyPheThrLeuGlnAsnValGlyArgIysSerGlySerGluThrProLeuProGlu	100		441	GlyHisGlyCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu	460
DB	751	CCCGCTTCACGCTCCAGAACGTGGGGCGCAATCCGGTCCGAGACGCGCTTCCGGAA	810		1831	GGTCATGGGAATGTTTGATGGACAAGCCTCAGANTCCCATACAGCTCCCGAGCGATCTC	1890
QY	101	ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla	120		461	ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerIys	480
DB	811	ACCGACTTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC	870		1891	CCTGGCACCTCGTAACGATGCCAACCGGCAGTGCAGTTTACATTGGGGAGGACTCCAAA	1950
QY	121	AlaLeuSerLeuGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe	140		481	HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly	500
DB	871	GCCCTCAGCCTCTGAGAGGGGTGGCGCGGCTTCTACCTGCTGGGGAGGCGGTATTTC	930		1951	CACCTGCCCGGATGCAGCCAGCACATGTAGCACCTTGTGTGTATCCGGCACCTCTGTGGGG	2010
QY	141	IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro	160		501	ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly	520
DB	931	ATCCAGCGCTGCCCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCGCGGAGAGCGC	990		2011	GTGCTGTGTGTCAACCAACACACTTCCCGTGGCGGATGGCACCCAGCTGTGGGAGAGGG	2070
QY	161	ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr	180		521	LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro	540
DB	991	CCGGCACCACTACAGTTCCACTCTCTCGCGGGAATCGCAGGGGAGCGTAGGGCGCAGC	1050		2071	AAATGGTGTATCAACGCGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTGATACGCTT	2130
QY	181	CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp	200		541	PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly	560
DB	1051	TGCGGGGTCTGGACGACGAGCGCCCGCGCTGCGGAAAGCGGAGACCGAAAGACGAGAC	1110		2131	TTTCATCGAAGCTGGGGAAATGTGGGGCTTGGGAGACTGTTCCGAAACGTGCGGTGGA	2190
QY	201	GluGlyThrGluGlyGluAspGlyProGlnTrpSerProGlnAspProAlaLeuGln	220		561	GlyValGlnTrpThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr	580
DB	1111	GAAGGAGCTGAGGGCGAGCGAAGGGCTCAGTGGTCCGCGCAGACCCCGCACTGCCAA	1170		2191	GGAGTCAGTACAGCATGAGGGAAATGTGAACCCAGTCCCAAGAAATGAGGGAAGTAC	2250
QY	221	GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis	240		581	CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn	600
DB	1171	GGCGTAGGACACCCACAGGAACCTGGAAGCATAGAAAGAGCGATTTGTCTCCAGTCAC	1230		2251	TGTGAAGGCAACCGAGTGGCTACAGATCTGTAAACCTTCAGGACTGTCCAGACAATAAT	2310
QY	241	ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly	260		601	GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe	620
DB	1231	CGCTATGTGGAACCATGCTTGTGGCAGACCATGCGATGGCAGAAATCCACGGCAGTGGT	1290		2311	GGAAAAACCTTTAGAGAGGAACAATGTGAAGCAACAACAGATTTTCAAAAGCTTCCTTT	2370
QY	261	LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer	280		621	GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg	640
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QY	281	IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys	300		641	CysLysLeuIleCysGlnAlaLysGlyIleGlyThrPhePheValLeuGlnProLysVal	660
DB	1351	ATTCTGTAATTCAGTTAGCTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAGA	1410		2431	TGCAAGCTCATCTGCCAAGCAAAAGGCATTTGGCTACTTCTTCGTTTTGCGAGCCCAAGTT	2490
QY	301	GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys	320		661	ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal	680
DB	1411	GGGCGGAAGTGACTCCATGCTCCCTCACTTCGCGAACTTTTGGAACTGGCAGGAAG	1470		2491	GTAGATGTAATCATGTAGCCAGATTCACCTCTCTCTGTGTGTGCAAGACAGTGTGTA	2550
QY	321	GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr	340		681	LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys	700
DB	1471	CAGCAACACCCACCCAGTGACCGGATGCAGAGCACTATGACACAGCAATCTTTTACC	1530		2551	AAAGCTGGTGTGTCATCGCATCATAGACTCCCAAAAGAAAGTTTGATAAATGTGTGTTCG	2610
QY	341	ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr	360		701	GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly	720
DB	1531	AGACAGGACTTGTGGGTGCCAGACATGTGATACTCTTGGGATGGCTGATGTGGAACT	1590		2611	GGGGAAATCGATCTACTTGTAAAAAATATCAGGATCAGTACTACTAGTCGAAACCTGGA	2670
QY	361	ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe	380		721	TyrHisAspIleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsn	740

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Db      2671 TATCATGATATCATCAATTCACCTGGAGCCACCAACATCGAAGTGAAACAGCGGAAC 2730
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      |||||
Db      2731 CAGAGGGATCCAGGAACAATGGCAGCTTCTTGGCCATCAAGCTCTGATGCACATAT 2790
QY      761  IleLeuAsnGlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrIysGlyVal 780
      |||||
Db      2791 ATTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGACAAAGTGTT 2850
QY      781  ValLeuArgTyrSerGlySerAlaAlaLeuGluArgIleArgSerPheSerProIleu 800
      |||||
Db      2851 GTCCTGAGGTACAGCGCTCTCTCGGCATTTGGAAGAAATTCGCAGCTTTAGCCCTCTC 2910
QY      801  LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProIysIleIys 820
      |||||
Db      2911 AAGAGCCCTTCACCATCCAGGCTCTTACTGTGGGCAATGCTCTCGACCTAAATTA 2970
QY      821  TyrThrTyrPheValIysIysIysGluSerPheAsnAlaIleProThrPheSerAla 840
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Db      2971 TACACCTACTCTGTAAGAGAGAGAGGAATCTTTCAATGCTATCCCACTTTTTCAGCA 3030
QY      841  TrpValIleGluGluTrpGlyGluCysSerIysSerCysGluLeuGlyTyrGlnArgArg 860
      |||||
Db      3031 TGGTCATTTGAAGAGTGGGGCGAATGTTCTAAGTCTATGTAATTGGTTGGCAGAGA 3090
QY      861  LeuValGluCysArgAspIleAsnGlnPheAlaSerGluCysAlaIysGluValIys 880
      |||||
Db      3091 CTGGTAGAATGCCAGACATTAATGCAGACCGCTGCTTCGAGTGTCCAAAGGAAGTGA 3150
QY      881  ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
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Db      3151 CCAGCCAGCACCAGACCTTGTGCAGACCATTCCTGCCCCAGTGCAGTGGGGAGTGG 3210
QY      901  SerSerCysSerLysThrCysGlyLysGlyTyrIysLysArgSerLeuIysCysLeuSer 920
      |||||
Db      3211 TCATCATGTTCTAGACCTGTGGGAAGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTCC 3270
QY      921  HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuIysLysProIysHisPhe 940
      |||||
Db      3271 CATGATGAGGGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAACATTT 3330
QY      941  IleAspPheCysThrMetAlaGluCysSer 950
      |||||
Db      3331 ATAGACTTTTGCACATGGCAGAAATGCAGT 3360

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RESULT 2

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US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(4858)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc feature
; LOCATION: (1)...(4858)
; OTHER INFORMATION: n = A,T,C or G
US-09-392-184-1

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Alignment Scores:

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Pred. No.: 0 Length: 4858
Score: 5176.00 Matches: 950
Percent Similarity: 99.89% Conservative: 0
Best Local Similarity: 99.89% Mismatches: 0
Query Match: 99.75% Indels: 1
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-392-184-1 (1-4858)

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Db      505  ATGGGAAACGGCGAGCGGGCTCCGGAGCTTTGGGCCCGTATACCCACGCTGTCTG 564
QY      21  LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerSerGluGluAsp 40
      |||||
Db      565  CTGCTCGCGCGCGCTACTGCGCGTGTGCGACGCACTCGGGCGGCCCTCCGAGGAGGAC 624
QY      41  GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrArgIleuArg 60
      |||||
Db      625  GAGGAGCTAGTGGTGGCGGAGCTGGAGCGGCCCGCGGACACGGGACCCACGCTCCGC 684
QY      61  LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
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Db      685  CTGCACGCTTTGACCGACGCTGATCTGAGGTGGCGCCCGCAGCAGCGCTTTTGGCG 744
QY      81  ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
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Db      745  CCGGCTTTCAGCTCCAGAAAGTGGGGCGCAATCCGGGTCCGAGACCGCGCTTCCGAA 804
QY      101  ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
      |||||
Db      805  ACCGCTTGGCGCACTGCTTCTACTCGGCACCGCTGAATGCGCATCCAGCTCGCTGCC 864
QY      121  AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrIleuLeuGlyGluAlaTyrPhe 140
      |||||
Db      865  GCGCTCAGCTCTCGAGGGCGTCCGGCGGCCCTTCTACCTGCTGGGGAGGCGCTATTTC 924
QY      141  IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysPro 160
      |||||
Db      925  ATCCAGCGCTGCGCGCGCGCGCGCGCTCCGCCACCGCGGCCCGCGGGGAGAAAGCCG 984
QY      161  ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
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Db      985  CCGGCACCACTACAGTTCCACCTCTCGGGCGGAATCGGCAGGGCGGCGTAGGGGGCAG 1044
QY      181  CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
      |||||
Db      1045  TCGGGGCTCGTGGACGACGAGCCCGCGCCGACTGGGAAAGCGGAGACCGAAGACGAGAC 1104
QY      201  GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
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Db      1105  GAAGGACTGAGGGCGGAGGAGGCGCTCAGTGTGCGCGCAGGACCCCGGCACTGCCAA 1164
QY      221  GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
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Db      1165  GGGCTAGACAGCCACAGGAACTGGGAAGCATAAGAAAGAACGATTGTGTGTCAGTCA 1224
QY      241  ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
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Db      1225  CGCTATGTGGAACCACTGCTTGTGGCAGACCACTGCGATGGCAGAAATTCACGGCAGT 1284
QY      261  LeuIysHisTyrIleuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrIysHisProse 280
      |||||
Db      1285  CTAAGCATTTACCTTCTCAAGCTTTGTTTCGTTGGCAGCCAGATTGTACAAACACCC 1344
QY      280  rIleArgAsnSerValSerLeuValValIysIleLeuValIleHisAspGluGlnIly 300
      |||||
Db      1345  CATTCGTAAATTCAGTTAGCTTGGTGGTGAAGATCTTGGTTCATCCACCATGAACAG 1404
QY      300  sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnIly 320
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Db      1405  GGGGCGGGAAGTGCCTCCATGCTGCCCTCACTCTGGGGAACCTTTTGCAACTGGCAG 1464

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QY 320 sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh 340
DB 1465 GAGCAACACCCAGGACCGGATGACAGGACATATGACAGCAATTCCTTTTCAC 1524
QY 340 rArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyTh 360
DB 1525 CAGACAGGACTTGTGTGGGTCCAGACATGTGATCTCTTGGGATGGCTGATGTGGAC 1584
QY 360 rValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPh 380
DB 1585 TGTGTGTGATCCGAGCAGAGGTGCTCCGTCATAGAGATGATGTTTACAAGCTGCCTT 1644
QY 380 eThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCy 400
DB 1645 CACCACAGCCCATGATTAAGCCACCTGTTTACATGCCATGATGATGCAAGCATG 1704
QY 400 salaserLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLe 420
DB 1705 TGCCAGCCTTAATGTGTGTGAATCAGGATTCACACATGATGGGTCAATTCCTTCCAACT 1764
QY 420 uAspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAs 440
DB 1765 GACACACAGCCAGCCTTGTCTCTCTGCAAGTCCATGATGATGATGATGATGATGAT 1824
QY 440 nGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLe 460
DB 1825 TGGTCATGGGGAATGTTTATGGAACAAGCTCAGATCCATACAGCTCCAGGCGATCT 1884
QY 460 uProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerIly 480
DB 1885 CCTTGACCTCGTACGATGCCAACCGGAGTGCAGATTTACATTTGGGGAGGATCCAA 1944
QY 480 sHisCysProAspAlaAlaserThrCysSerThrLeuTrpCysThrGlyThrSerGlyGl 500
DB 1945 ACACCTGCCCTGATGAGCCAGCACATGATGACCTTGTGTGTACCGGACCTCTGGTGG 2004
QY 500 yValleuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGl 520
DB 2005 GGTGTGTGTGTGTCACAAACCAACCTTCCGCTGGCGGATGGCACAGCTGTGGAGAAG 2064
QY 520 yLysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPr 540
DB 2065 GAAATGTGTATACACGCAAGTGTGTGACAAACCCAGACAAAGCAATTTTGTATGCC 2124
QY 540 oPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGl 560
DB 2125 TTTTCATGGAAGCTGGGGAATGTGGGGCTTGGGGACCTGTTCCAGAACGTGGGTGG 2184
QY 560 yGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTy 580
DB 2185 AGGAGTCCAGTACAGATGAGGAAATGCAACCCAGTCCCAAGAAATGGAGGAAGTA 2244
QY 580 rCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAs 600
DB 2245 CTGTGAAGGCAACAGGTGCTACAGATCTGTAACTTCCAGGACCTGTCCAGACATAA 2304
QY 600 nGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPh 620
DB 2305 TGGAAACCTTTAGAGAGGAACCAATGTGAAGCACAACCAAGTTCCTTCAAAAGCTTCTCT 2364
QY 620 eGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspAr 640
DB 2365 TGGAGTGGGCTGCTGGGTGAATGGAATTCCTCCAGTACCTGCTCCACCAAGAGCAG 2424
QY 640 qCysLysLeuIleCysGlnAlaLysGlyIleGlyThrPhePheValleuGlnProLysVa 660
DB 2425 GTGCAAGCTCATCTGCCAAGCAAGGCATTTGGTACTTCTTCTTGTGGCCCAAGGT 2484
QY 660 lValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlnCysVa 680
DB 2485 TGTAGATGGTACTCCATGATGCCAGATTCACCTCTGTCTGTGTGAGGACAGTGTGT 2544
QY 680 lLysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCy 700

DB 2545 AAAAGCTGTTGTGATCGCATCATAGACTCCAAAAGAAAGTTTGTATAATGTGTGTGTG 2604
QY 700 sGlyGlyAsnGlySerThrCysLysLysLysLysLysLysLysLysLysLysLysLys 720
DB 2605 CGGGGAAATGGATCTACTTGTATAAATAATCAGGATCAGTTACTGTGCAAAACCTGG 2664
QY 720 yYHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAs 740
DB 2665 ATATCATGATATCATCAATTCACATTCGAACTGGAGCCACCAACATCGAAGTGAACGCGAA 2724
QY 740 nGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTy 760
DB 2725 CAGAGGGGATCCAGGAACAATGGCAGCTTCTTGGCCATCAAGCTGTGTGAGGCACATA 2784
QY 760 rIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVa 780
DB 2785 TATCTTAAATGCTGACTACACTTGTCCACCTTAGAGCAAGACATTTATGTACAAAGTGT 2844
QY 780 lValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLe 800
DB 2845 TGTCTTAGGTACAGCGCTCTCTCGGGCATTCGGAAGAATTCGACGCTTTAGCCCTCT 2904
QY 800 uLysGlyProLeuThrIleGlnValLeuThrValGlyAsnAlaAlaLeuArgProLysIleLy 820
DB 2905 CAAGAGCCCTTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCACCTAAATTA 2964
QY 820 sTyrThrTyrPheValLysLysLysLysLysLysLysLysLysLysLysLysLys 840
DB 2965 ATACACCTACTTCTGTAAGAAGAAAGAAAGAAATCTTTCAATGCTATCCCACTTTTCAGC 3024
QY 840 aTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgAr 860
DB 3025 ATGGGTCAATGAAGAGTGGGGCGAATGTTCTAAGTCATGTGATGGTGGCAGAGAG 3084
QY 860 gLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluVally 880
DB 3085 ACTGTTAGAATGCCAGACATTAATGACAGCCTGCTCCGAGTGTGCAAAAGAAAGTAA 3144
QY 880 sProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTr 900
DB 3145 GCCAGCAGCACACAGACCTTGTGCAGACCACTCCCTGCCCGCAGTGGCGAGGTG 3204
QY 900 pSerSerCysSerLysThrCysGlyLysGlyLysLysLysLysLysLysLysLysLys 920
DB 3205 GTCATCATGTTCTAAGACCTGTGGAGGTTTACAAAAAGAAAGCTTGAAGTGTCTGTC 3264
QY 920 xHisAspGlyGlyValleuSerHisGluSerCysAspProLeuLysLysProLysHisPh 940
DB 3265 CCATGATGGAGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTTAACATTT 3324
QY 940 eIleAspPheCysThrMetAlaGluCysSer 950
DB 3325 CATAGACTTTTGCAATGGCAGATGCACT 3355

RESULT 3

US-09-568-559-1

; Sequence 1, Application US/09568559

; Patent No. 6649377

; GENERAL INFORMATION:

; APPLICANT: Klonowski, Paul

; APPLICANT: Allard, John

; APPLICANT: Heller, Renu

; APPLICANT: van Wart, Harold

; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid

; FILE REFERENCE: ROCH-002

; CURRENT APPLICATION NUMBER: US/09/568,559

; PRIOR FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: 60/133,343

; PRIOR FILING DATE: 1999-05-10

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

! SEQ ID NO 1
! LENGTH: 3889
! TYPE: DNA
! ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.: 0 Length: 3889
Score: 5174.00 Matches: 948
Percent Similarity: 99.79% Conservative: 2
Best Local Similarity: 99.79% Mismatches: 0
Query Match: 99.71% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-568-559-1 (1-3889)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
DB 59 ATGGGGAACCGGAGCGGGCTCCGGGCTCTCGAGCTTTGGGCGGTACCCACGCTGCTG 118
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
DB 119 CTGCTCGCCGCGGCGCTACTGGCGGTGTGAGCGCACTCGGGCGCCCTCCGAGGAGAC 178
QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
DB 179 GAGGAGCTAGTGTGCTCCGAGCTGGAGCGCGCCCGGAGACCGGACCGGCTCCGC 238
QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerPheLeuAla 80
DB 239 CTGACACGCTTTGACACGACGCTGGATCTGGAGCTGCGGCGCGACAGCAGCTTTTGGCG 298
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerGluThrProLeuProGlu 100
DB 299 CCGGCTTCACGCTCCAGACGTTGGGCGCAATCCGGGTCCGAGACCGCGCTTCGGAA 358
QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
DB 359 ACCGACCTGCGCACTCTTCTACTCCGCGCACCGTGAATCGCGATCCAGCTCGGCTGCC 418
QY 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
DB 419 GCGCTCAGCTCTGCGAGGGCGTGGCGGCGCTTCTACCTGCTGGGGAGGCGTATTTC 478
QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
DB 479 ATCCAGCGCTGCCCGCGCCGCGAGCGCTCGCCACCGCGCCCGCGGAGAGCGG 538
QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180
DB 539 CCGGCACTACAGTTTCCACCTCTCGCGCGGAAATCGGAGGCGGACGTCGCGGCGCAG 598
QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
DB 599 TCGGGGTCTGACGACGAGCGCCCGCGCGCTCGGAAAGCGGAGACCGAAGACGAGGAC 658
QY 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
DB 659 GAAGGACTCAGGCGGAGGACGAAGGGGCTCAGTGTGTCGCGGAGCACCGGCACTGCAA 718
QY 221 GlyValGlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHis 240
DB 719 GCGGTAGCAGGCCCAAGAACTGGAAGCATAGAAAGGCGATTTGTCCAGTCAC 778
QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
DB 779 GGTATGTGGAACCATGCTTGTGGCAGACCATGTCGATGCGAGAAATTCACGCGCAGTGT 838
QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
DB 839 CTAAGCAATACCTCTCAGCTTGTTCGCTGGCAGCCGACGATTTGTACAAACACCCGAC 898
QY 281 IleArgAsnSerValSerLeuValValLysIleLeuValLysIleHisAspGluGlnLys 300

DB 899 ATTCTGTAATTCTAGCTTGGTGGTGAAGATCTTGGTTCATCCACGATGACAGAAG 958
QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
DB 959 GGGCCGGAAGTGACCTCCAAATGCTGCCCTCCTCTCGGAACCTTTGCAACTGGCAAG 1018
QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
DB 1019 CAGCACAAACCCAGTACCGGATGACCGGATGACAGCACTATGACACAGCAATCTTTTACC 1078
QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
DB 1079 AGACAGACTTGTGTGGGTCCGACAGCATGTGATCTCTTGGGATGGCTGATGTGGAAT 1138
QY 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaIlePhe 380
DB 1139 GTGTGTGATCCGAGCAGAGAAGCTCTCCGTCATAGAGATGATGTTTACAAGCTGCTTC 1198
QY 381 ThrThrAlaHisIleLeuLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
DB 1199 ACCACAGCCCATGAATAGGCCACGCTTTTAAATCATGACGCACTGATGATGATGATGAT 1258
QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
DB 1259 GCCAGCTTTAATGGTGTGAACAGGATTCACCATGATGCGCTCAATGCTTCCAACTG 1318
QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
DB 1319 GACCACAGCAGCTTGGTCTCTCTTGCAGTGGCTACATGATTTACATCATTTCTGGGTAAT 1378
QY 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
DB 1379 GGTATGGGGAATGTTGATGGACAGCTCAGATCCCATACAGCTCCAGGCGATCTC 1438
QY 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
DB 1439 CCGTGGCAGCTCTGATCGATGCCAACCGGAGTGCAGTTTACATTTGGGGAGGACTCCAA 1498
QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
DB 1499 CACTGCCCCCTGATGACCGCAGCAGCATGTAGACCTTGTGTGTGTACCGGACCTCTGTGG 1558
QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
DB 1559 GTGCTGTGTGTCAACCAACACATTCCTCGGGCGGATGGCACCAGCTGTGGAGAAGGG 1618
QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
DB 1619 AAATGTGTATCAACGGCAAGTGTGTGAACCAAAACCCACAGAAAGCATTTTGTATACGCT 1678
QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
DB 1679 TTTTCATGGAGCTGGGGAATGTGGGGCTTGGGGAGACTGTTTCGAGAACGTGGGTGGA 1738
QY 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
DB 1739 GGAGTCCAGTACACCATGAGGGAATGTGAACCCAGTCCCAAGAAATGGAGAAAGTAC 1798
QY 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
DB 1799 TGTGAAGGCAACAGGTGCGCTACAGATCTGTAACTTGGAGACTGTCCAGCAATAAT 1858
QY 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
DB 1859 GGAAAAACCTTTAGAGAGGAACAAATGTGAAGCACACACAGAGTTTCAAAGCTTCTCTT 1918
QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
DB 1919 GGGAGTGGGCGCTCGCGTGAATGGATTTCCAGTAGTACCTGGCGCTCTCAACAAAGGACAG 1978
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660

Db 1979 TCAAGCTCATCTGCCAAGCCAAAGCATGTGGCTACTTCTTGTTTTCAGCCCAAGGTT 2038
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValcLbGlyGlnCysVal 680
Db 2039 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGCTGTGTGTCAGGACAGTGTGTA 2098
QY 681 LysAlaGlyCysAspArgIleileAspSerLysLysPheAspLysCysGlyValCys 700
Db 2099 AAGCTGGTGTGTGATCGCATCATGACTCCAAAAGAGTGTGATAAATGTGGTGTTC 2158
QY 701 GlyGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGly 720
Db 2159 GGGGGAATGATCTACTGTGTAATAAATATATCAGATCAGTTACTAGTGCAAAACCTGGA 2218
QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db 2219 TATCATGATATATCATCAAAATTCACCTGGAGCCACCAACATCGAAGTGAACAGCGGAAC 2278
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAspGlyThrTyr 760
Db 2279 CAGAGGGATCCAGGACATAGGCGAGCTTCTTGCCATCAAGCTCTCATGGCACATAT 2338
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db 2339 ATTCTTAATGGTGTACTACACTTGTCCACCTTAGAGCAAGACATATATGACAAAAGTGT 2398
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
Db 2399 GTCITGAGGTACAGCGGCTCTCTGCGCATTTGGAAGATTCGAGCTTTAGGCCCTCTC 2458
QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
Db 2459 AAAGAGCCCTTGACCATCCAGTCTTACTGTGGCAATGCCCCTTCGACCTTAAATTA 2518
QY 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db 2519 TACACCTACTCTGTAAGAGAGAGAGGAATCTTTCATGCTATCCCCACCTTTTCGCA 2578
QY 841 TrpValIleGluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
Db 2579 TGGTCTATTGAAGATGGGGGGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAGA 2638
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
Db 2639 CTGTAGATGCCAGACATTAATGGACAGCTCTCTCCGAGTGTGCAAAAGAGTGAAG 2698
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db 2699 CCAGCCAGCACACACCTTGTGCGAGACATCCCTGCCCCAGTGGCAGCTGGGGGAGTGG 2758
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
Db 2759 TCATCATGTTCTTAAGACTGTGGGAGGGTTACAAAAGAGAGCTTGAAGTGTCTGTCC 2818
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db 2819 CATGATGGAGGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTAAACATTC 2878
QY 941 IleAspPheCysThrMetAlaGluCysSer 950
Db 2879 ATACACTTTTGCAATATGGCAGATGCACT 2908

RESULT 4

US-09-484-970B-58
; Sequence 58, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmer, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B

; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 007074.1
; NAME/KEY: unsure
; LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3664, 3674, 3681
; OTHER INFORMATION: a, c, g, or other
US-09-484-970B-58

Alignment Scores:

Pred. No.: 0 Length: 3706
Score: 4287.00 Matches: 777
Percent Similarity: 99.87% Conservative: 0
Best Local Similarity: 99.87% Mismatches: 0
Query Match: 82.62% Indels: 1
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-484-970B-58 (1-3706)

QY 174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193
Db 3 CAGGGCACGTAGCGGCACGTGCGGGTCTGTGGACGACGAGCCCGCGACTGGGAAA 62
QY 194 AlaGluThrGluAspGluAspGluGlyThrGluGlyLysAspGluGlyProGlnTrpSer 213
Db 63 GCGGAGACCGAAGACGAGGAGCGAAGGACTGAGGGCGGAGGAGCGAGGCTGCTG 122
QY 214 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 233
Db 123 CCGCAGGACCGCGACCTGCAAGCGCTAGGACAGCCACAGGAACTGGAAGCATAGAA 182
QY 234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253
Db 183 AAGCGATTTGTGTCAGTCAACCGCTATGTGGAAACCATGCTTGTGCGACAGCATG 242
QY 254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 273
Db 243 GCAGAATTCACGCGCAGTGTCTAAAGCATTAACCTCTCACGTTGTTTCGGTGGCAG 302
QY 274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu 293
Db 303 AGATTGTACAAACCCCGACATTCGTAATTCAGTTAGCTGTGTGTGTGAAGATCTTG 362
QY 294 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 313
Db 363 GTCATCCAGATGAACAGAAAGGGCGGGAAGTGACCTCCAAATGCTGCCCTCACTCTG 422
QY 314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333
Db 423 AACTTTTGCACTGGCAGAGAGCAGACAAACCCAGTGACCGGATGACAGAGCACTAT 482
QY 334 AspThrAlaIleLeuPheThrArgGlnAspLeuLysGlySerGlnThrCysAspThrLeu 353
Db 483 GACACAGCAATCTTTTCCACAGACAGAGCTTGTGTGGCTGCCAGACATGTGATACTCT 542
QY 354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373
Db 543 GGGATGGCTGATGTGTGAACCTGTGTGTATCCGACAGAGAGCTGCTCCGTCTAGAGAT 602
QY 374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393
Db 603 GATGTTTACAGCTGCCTTCCACACGCCCATGATTAAGGCCAGCTGTTTAACATGCCA 662
QY 394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413
Db 663 CATGATGATGCAAGCAGTGTGCCAGCTTATGTGTGTGAACAGGATTTCCACATGATG 722

QY 414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTyrProCysSerAlaTyrMet 433
 DB 723 GCCTCATGCTTCCAACTGGACACAGCCCTTGGTCTCTTGCAGTGGCTACATG 782
 QY 434 IleThrSerPheLeuAspGlnGlyHisGlyGluCysLeuMetAspGlnPro 453
 DB 783 ATTACATCATTTCTGGATATGCTGATGGGAATGTTGATGACCAAGCTCAGAATCC 842
 QY 454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473
 DB 843 ATACAGCTCCAGCGCATCTCCCTGGACCTCTGATGATGCCAACCGGAGTGGCAGTTT 902
 QY 474 ThrPheGlyCysAspSerLysHisCysProAspAlaAsnSerThrCysSerThrLeuTyr 493
 DB 903 ACATTTGGGAGGACTCCAAACACTCCCGCATGTCAGCCAGCACATGTAGCACCTTGTGG 962
 QY 494 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTyrAlaAsp 513
 DB 963 TGTACCGGACCTCTCTGGTGGGGTGGTGGTGTGCAACCAACCAACACTTCCCGTGGGGGAT 1022
 QY 514 GlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysThrAsp 533
 DB 1023 GGACACGCTGTGGAGAGGGAATGTGTATCAACGGCAAGTGTGTGAACAACCGAC 1082
 QY 534 ArgLysHisPheAspThrProPheHisGlySerTyrProGlyMetTyrProTyrGlyAsp 553
 DB 1083 AGAAACATTTTCATACGCTTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGAC 1142
 QY 554 CysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 573
 DB 1143 TGTTCGAGAACTGCGTGGAGAGTCCAGTACAGATGAGGGATGTGCAACCACTGTC 1202
 QY 574 ProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 593
 DB 1203 CCAAGAAATGGAGGAAGTACTGTGAAGGCACAAACGAGTGGCTTACAGATCTCTGTAACTT 1262
 QY 594 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluCysGluAlaHisen 613
 DB 1263 GAGGACTGTCCAGACATTAATGAAACCTTTTAGAGAGGAACAATGTGAAGCACACAC 1322
 QY 614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPheProLysTyrAla 633
 DB 1323 GAGTGTTCAAAAGCTTCCTTTGGAGTGGGCTGGGTGGATGGATGCCCAAGTAGCT 1382
 QY 634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 653
 DB 1383 GGCGTCTCAAAAGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCAATGGCTACTTC 1442
 QY 654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673
 DB 1443 TTGGTTTTCAGCCCAAGTGTAGTGTGTACTCCCATGTAGCCAGATTCACCTCTGTC 1502
 QY 674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleAlaAspSerLysLys 693
 DB 1503 TGTGTCAAGGACAGTGTGTAAGCTGGTGTGTGATCGCATCATAGACTCCCAAAAGAG 1562
 QY 694 PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySer 713
 DB 1563 TTGTATAATGTGGTGTTCGGGGGAATGATCTACTTTGTAATAAATAATACAGATCA 1622
 QY 714 ValThrSerAlaLysProGlyTyrHisAspIleThrIleProThrGlyValaThrAsn 733
 DB 1623 GTTACTAGTCAAAACCTCGATATCATGATATCATCAAAATCCAACTGGAGCCACCAAC 1682
 QY 734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 753
 DB 1683 ATCGAAGTGAACACGCGGAACAGAGGGGATCCAGGAACAATGGGCAGCTTCTTGGCAT 1742
 QY 753 elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGly 773
 DB 1743 CAAGCTCTGTGGCACAATATTTCTTAATGTGACTACACTTGTGCCACCTTAGACCA 1802
 QY 773 naspileMetTyrLysGlyValValLeuArgTyrSerGlySerAlaAlaLeuGluArg 793

DB 1803 AGACATTATGACAAAGGTGTGTCTTGGGTACAGGGCTCTCTCTGGGCAATGGAAAG 1862
 QY 793 gileArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 813
 DB 1863 AATTCGCAGCTTTAGCCCTCTCAAGAGAGCCCTTGACCATCCAGGTCTTTACTGTGGCAA 1922
 QY 813 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGluSerPheAs 833
 DB 1923 TGCCCTTCGACCTTAATTAATACACCTTCTCTGAAGAAGAAGAAGAAATCTTTCA 1982
 QY 833 nAlaIleProThrPheSerAlaTyrValIleGluGluTyrGlyGluCysSerLysSerCy 853
 DB 1983 TGCTATCCCACTTTTTCAGCATGGCTCAATGAAGAGTGGGCGAATGTCTTAAGTCATG 2042
 QY 853 sGluLeuGlyTyrGlnArgArgLeuValGlyCysArgAspIleAsnGlyGlnProAla 873
 DB 2043 TGAATGTGGTGGCAGAGAGACTGTGTAAATGCCGAGACATTAATGGACGCCCTTC 2102
 QY 873 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 893
 DB 2103 CGAGTGTCCAAAGGAAGTGAAGCCAGCCAGCCAGACCTTGTGCAGACCATCCCTGCC 2162
 QY 893 oGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLy 913
 DB 2163 CCAGTGGCAGCTGGGGAGTGTGTATCATGTCTTAAGACCTGTGGGAAGGGTTACAAA 2222
 QY 913 sArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAspPr 933
 DB 2223 AAGAAGCTTGAAGTGTCTGTCCCATGTGGAGGGGTGTATCTCATGAGAGCTGTGATCC 2282
 QY 933 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
 DB 2283 TTTAAGAAACCTTAACATTTTCATAGACTTTTGACAAATGGCAGAAATGCAGT 2334

RESULT 5

US-09-445-023A-2
 ; Sequence 2, Application US/09445023A
 ; Patent No. 6563858
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirose, Kunitaka
 ; APPLICANT: Inoguchi, Eiji
 ; APPLICANT: Hakozaki, Michinori
 ; APPLICANT: Ishioka, Keiko
 ; APPLICANT: Ishida, Yukako
 ; APPLICANT: Matsushima, Kouji
 ; APPLICANT: Kuno, Kouji
 ; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
 ; FILE REFERENCE: Q57092
 ; CURRENT APPLICATION NUMBER: US/09/445,023A
 ; CURRENT FILING DATE: 1999-12-03
 ; PRIOR APPLICATION NUMBER: JP 9-160422
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 2184
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (1)..(2184)
 US-09-445-023A-2

Alignment Scores:
 Pred. No.: 0 Length: 2184
 Score: 3947.00 Matches: 712
 Percent Similarity: 99.44% Conservative: 4
 Best Local Similarity: 98.89% Mismatches: 4
 Query Match: 76.06% Indels: 0
 Gaps: 4
 DB:


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RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Harose, Kunitaka
; APPLICANT: Inoguchi, Ei-ji
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.: 0 Length: 2184
Score: 3677.00 Matches: 651
Percent Similarity: 95.32% Conservative: 42
Best Local Similarity: 89.55% Mismatches: 34
Query Match: 70.86% Indels: 0
DB: 4 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-445-023A-13 (1-2184)
QY 224 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerHisArgTyrVal 243
DB 1 AAGCCATCAGGACGAGGATAGGAGAGGATTTGTGTCCAGCCCGGTTATGTG 60
QY 244 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 263
DB 61 GAAACCATGCTGTAGTCCAGGCTCATGGCCGCTTCCAGGAGCGGCTTAAGGAT 120
QY 264 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 283
DB 121 TACCTTCTAACCTGTCTCTCGTGGCAGCCAGGTTTACAGCATCCAGCATTAGGAAT 180
QY 284 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 303
DB 181 TCAATTAGCTGTGTGTGTGAAGATCTTGGTATATACGAGGAGCAGAGGACAGAA 240
QY 304 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 323
DB 241 GTTACCTCCATGCGAGCTCTACCTTCGGATTTCTGAGCTGGCAGGAGGAGGAGGAGG 300
QY 324 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 343
DB 301 AGCCCCAGTGACCGGATCCAGAGCACTATGACACTGCAATTTCTGTTCACAGCAGGAT 360
QY 344 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 363
DB 361 TTATGTGGCTCCACAGCTGTGACATCTCGGATAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 364 ProSerArgSerCysSerValIleGluAspAspGlyLeuGluAlaAlaPheThrThrAla 383
DB 421 CCCAGCAGGAGCTGCTCAGTGCATAGAGATGATGTTTGCAGAGTGCCTTCCACAGGCC 480
QY 384 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 403
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481 CATGAATTGGGCCCATGTGTTAAACATGCGCAGATGATGCTTAAGCACTGTGCCAGCTTG 540
QY 404 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 423
DB 541 AATGGTGTGAGTGGCGATTCTCACTGATGGCTCGATGCTCTCCAGCTTAGACCATAGC 600
QY 424 GlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsnGlyHisGly 443
DB 601 CAGCCCTGGTCACTTGCAGTGCCTTACATGCTGCTTCTTCTAGATTAATGACACGG 660
QY 444 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 463
DB 661 GAATGTTTGAATGAGCAACGCCGAGATCCATCAAGCTCCCTTCTGATCTTCCCGGTACC 720
QY 464 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 483
DB 721 TTGTAGCATGCCAACCGCAGTGTCACTTTCATTCGGAGAGGAATCAAGCACTGCCCT 780
QY 484 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyVal 503
DB 781 GATGAGCAGCAGCATGATGATACCTGTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 504 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 523
DB 841 TGCCAAACAAACACTTCCCTTGGCAGATGGCAGCTGTGGAGAGGAGGAGGAGTGTGT 900
QY 524 IleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrProPheHisGly 543
DB 901 GTCAGTGGCAAGTGTGCTGCAACCAAGACATGATGAGCATTTTGTCTACTCTCTTCA 960
QY 544 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 563
DB 961 AGCTGGGACCATTTGGGACCGTGGGAGACTGCTCAGAACCTGTGTGGTGGGAGTTCNA 1020
QY 564 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly 583
DB 1021 TACCAATGAGAGATGTGACAAACCCAGTCCCAAGAAACGAGGAGGAGTACTGTGAAGC 1080
QY 584 LysArgValAlaGlyTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnLysThr 603
DB 1081 AAACAGAGTCCCTACAGGTCTGTAACTCAGGAGCTCTCCAGCAATTAACCGAAAGAG 1140
QY 604 PheArgGluGlnGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 623
DB 1141 TTCAGAGGAGGAGGAGTGGAGGCGCACAAATGAGTTTCCAAAGCTTCTTTGGGAATGAG 1200
QY 624 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 643
DB 1201 CCCACTGTAGAGTGGACACCCCAAGTACCGCGCGCTCGCCAAAGGACAGGTCAGGCTC 1260
QY 644 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 663
DB 1261 ACCGTGGAAGCCAAAGGATTTGGCTACTTTTGTCTTACAGCCCAAGGTTGTAGATGC 1320
QY 664 ThrProCysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGly 683
DB 1321 ACTCCCTGTAGTCCAGACTCTACCTCTGTGTGTGCAAGGCGAGTGTGTGAAGCTGGC 1380
QY 684 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 703
DB 1381 TGTATGTCATCATAGACTCCAAAGAAAGTTTGTATAGTGTGGCGTTTGTGGAGAAAC 1440
QY 704 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 723
DB 1441 GGTTCACATCCAGAGAGATGTCAGGATAGTACTAGTACAGACCTGGGTATCATGAC 1500
QY 724 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 743
DB 1501 ATTGTCACAATTCCTGTGGAGCCCAACCAATTAAGTGAACATCGGAATCAAGAGGGG 1560
QY 744 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 763
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Db 1561 TCCAGAACCAATGCGAGCTTTCTGGCTATTAGAGCCGCTGATGTAACCTATATCTGAAT 1620
Qy 764 GlyAspTyrThrLeuSerThrLeuGluAspIleMetTyrLysGlyValValLeuArg 783
Db 1621 GGAACCTTCACTCTGTCCAGACTAGACAGACCTTCACTACAAAGAGTACTGCTTAAGG 1680
Qy 784 TyrSerGlySerSerAlaLeuLeuGluArgIleArgSerPheSerProLeuLysGluPro 803
Db 1681 TACAGTGGTTCTCTGGCTGGCTGGAAAGAAATCGCAGCTTTAGTCCACTCAAGAACCC 1740
Qy 804 LeuThrIleGlnValLeuThrValGlyValAlaLeuArgProLysIleLysTyrThrTyr 823
Db 1741 TTAACCATCCAGGTTCTATGGTAGGCTCTCTCCGACCCAAATTAATTCRCCTAC 1800
Qy 824 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 843
Db 1801 TTTATGAAGAAGAACAGACAGACTCATTCACGCCATTCGCCATTTCTGAGTGGTGATT 1860
Qy 844 GluGlnTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 863
Db 1861 GAAAGTGGGGGAGTGTCTCAAGACATGCGGCTCAGGTTGGCAGAGAGTAGTGCAG 1920
Qy 864 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 883
Db 1921 TGCAGAGACATTAACGACACCTCTCTCCGAATGTGCAAGGAAGTGAAGCCAGCCAGT 1980
Qy 884 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 903
Db 1981 ACCAGACCTTGTGCAGACCTTCTCTTGCCACACTGGCAGGTGGGGGATTTGGTCAACCAT 2040
Qy 904 SerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSerHisAspGly 923
Db 2041 TCCAAACTTCGGGAGAGGTTACAGAGAGAACCTTGAATGTGTGCCACGATGGG 2100
Qy 924 GlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPheIleAspPhe 943
Db 2101 GGCCTGTATCAATAGAGCTGTGATCTTTTGAAGAAGCCAAAGCATTTACATTTGACTTT 2160
Qy 944 CysThrMetAlaGluCysSer 950
Db 2161 TGCACATGACACAGTGCAGT 2181

RESULT 7
US-09-369-364A-8
; Sequence 8, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3638
; TYPE: DNA
; ORGANISM: Mus musculus ADAMTS-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (278)..(2952)
; NAME/KEY: misc feature
; LOCATION: (3636)
; OTHER INFORMATION: n = T
US-09-369-364A-8
Alignment Scores:
Pred. No.: 8.44e-201 Length: 3638
Score: 2284.50 Matches: 449
Percent Similarity: 63.10% Conservative: 146
Best Local Similarity: 47.61% Mismatches: 265

Query Match: 44.03% Indels: 83
DB: 4 Gaps: 21
US-09-373-658C-2 (1-950) x US-09-369-364A-8 (1-3638)
Qy 17 ProThrLeuLeuLeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgPro 36
Db 308 CCGCCCTCTCTGCTGCTATTTCAGCTGCGCGCCGCCACTCTCTCTGCGGAGCCCG 367
Qy 37 Ser-----GluGluAspGluGluLeuValValProGluLeuGluArgAla 51
Db 368 GCGGGCGCGGACCGCGGCGCGAGCTCGGAGCTAGTGTGCCC-----ACGCGGTG 421
Qy 52 ProGlyHisGlyThr---ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeu 70
Db 422 CCGCGCAGCGCGAGCAGCAGCTTCCTCCACTTTCGCGCTTCGCGCAGGCTTCGCTG 481
Qy 71 GluLeuArgProAspSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArg 90
Db 482 CGCTTGGCCCTGTCGCCAGCTTCTTGGCGCCCGAATTCAAGATCGAGCGCTCGGGGC 541
Qy 91 LysSerGlySerGluThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGly 110
Db 542 TCGAGCGCGCGCGCGG-----GGCAGCGCGGAGCTGCGTGGCTCTCTCTCTGCG 595
Qy 111 ThrValAsnGlyAspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGly 130
Db 596 ACAGTGAATGGAACCGGAGTCTGCGCGCGCATGAGCTGTGTCGCGGCTCGAGCGCG 655
Qy 131 AlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer----- 148
Db 656 TCGTCTCTGCGCAGCGCGAGGATTCACATCCAGCCACAGGGCGCTGGGACTCCCTG 715
Qy 149 -----GluArgLeuAlaThrAlaAlaProGlyGluLysPro----- 160
Db 716 GACACGCTCATCGCTGCGAGCGCTGGGGCGCGGACAGCGCGCGAAGACCCCGGGCTC 775
Qy 161 -----ProAlaProLeuGlnPheHisLeuLeuArgAsn 172
Db 776 GCTCGCGCGGAGCTTTCCCTCCCTCAAGGACTGGAGTGGGAGGTGGAGATGGGTAAT 835
Qy 173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192
Db 836 GCGCAGGAGCAG----- 847
Qy 193 LysAlaGluThrGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212
Db 848 -----GAGAGAGTGCACACGAGAGAGGACAGACGAGCAGGAGGGGTGCTCAA 901
Qy 213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232
Db 902 GAGACAGAGACTCC-----CGCAAAGTCCACACCCCTTCGGATCC---AAAACTAGA 952
Qy 233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252
Db 953 AGCAGAGGTTTGTGTCGAGGCTCGCTTCGTGGAAACACTTCTGTGCTGATGCTGCC 1012
Qy 253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272
Db 1013 ATGGCTGCTTCTATGGAGCCGACCTTCAGAACACCATCTCACCGTGTGTCAATGGCA 1072
Qy 273 AlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIle 292
Db 1073 GCCCGAATCTACAAGCACCAGCAGCATCAGGAATCTCGTCAACCTTGTGGTGGTGAAGTG 1132
Qy 293 LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu 312
Db 1133 CTATAGTGGAAAAAGAGATGGGCGCGGAGTGTCCGACACCGGGGGCTCACACTG 1192
Qy 313 ArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis 332
Db 1193 CGCAACTTCTGACGTGGCAACGGCGCTTTTCAACAGGCCCGAGTGACCGCCCGGAGCAC 1252

333 TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGly---SerGlnThrCysAsp 351
1253 TATGACACTGCCATCTTTTCCACGACAGACTTCTGTGGAGGAGGAGGAGTGTGAC 1312
352 ThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIle 371
1313 ACCCTGGGATGCGACAGCTGTGCACCATCTGTGACCCCGACAGAGAGCTGTCTGATG 1372
372 GluAspAspGlyLeuGlnAlaPheThrThrAlaHisGluLeuGlyHisValPheAsn 391
1373 AAGGATGAGGAGCTGAGGAGCTACACCTGTGGCCATGAGTACGAGGACGCTTCTCAGC 1432
392 MetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHis 411
1433 ATGCCCATGATGATTAAGCCCTGTGTGAGATTGTTTGGGCCCATGGGCAAGTACCAC 1492
412 MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProThrSerProCysSerAla 431
1493 ATGATGGCCCATTTCTTCCATCCAGCGAAGACAGCTGCCCTGGTCTCCCTGCGATGCT 1552
432 TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln 451
1553 GNTACCTCACAGAGCTCTGGATGATGTCACGAGATTGCTTCTGATCCCCACC 1612
452 AsnProIleGlnLeuProGlyAspLeuProGly-----ThrSerTyrAspAlaAsnArg 469
1613 TCGGTTCTGCCCTCCCAAGAGCTCCCGGCGCACAGCACCTCTTACGAGCTGGACCAG 1672
470 GlnCysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAla-----Ser 487
1673 CAGTGCAGCAGATCTTGGGCTGATTTCCGACACTGCGCCCAACACCTCTGTGGAGAC 1732
488 ThrCysSerThrLeuTrpCysThrGlyThrSerGlyValValLeuValCysGlnThrLys 507
1733 ATCTGTCTCAGCTCTGCCCTGATCGGGATGATGATGATGATGATGATGATGATGAT 1792
508 His-----PheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsn 525
1793 AATGTAGCTCTCTGGGCTGATGATACCTCTGGCCCTGGGCACTGTGCTGCTGAT 1852
526 GlyLysCysValAsnLysThrAspArgLysHisPheAspThrProPheHisGlySerTrp 545
1853 GCTAGCTGTGTACTCAAGGAGATGAGGATGATGATGATGATGATGATGATGATGAT 1912
546 GlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGlnThrThr 565
1913 GGTCTCTGGAGACCTCGGGCAATGTTCTCGACACTGTGTGGAGGATACAAATCTCG 1972
566 MetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGlyLysArg 585
1973 AACCTGTGATGTGATATCCATGCTCAGATGAGGAGGATTTTCTGGTGGTGAAGA 2032
586 ValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArg 605
2033 GTCAAGTACCAATCATGCAACACAGAGGAATGCCACCA--AACGAAAAAGCTTCGG 2089
606 GluGlnGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerCysProAla 625
2090 GAGCAGAGTGGAGAAAT 2146
626 ValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCys 645
2147 CTGCACTGGGTCCTCCCAAGTATTCAGAGGTGTCCTCCCGGAGACCGATGCAAGCTTTTGC 2206
646 GlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrPro 665
2207 AGAGCCCTGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2266
666 CysSerProAspSerThrSerValCysValGlnGlnCysValLysAlaGlyCysAsp 685
2267 TGTGACCGGATACCTCTGTCATCTGCTCGGGGGCAATGTTTGAAGCTGCTGTGAC 2326
686 ArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySer 705

2327 CATGTGGTGAATCACTACCTAAGAGCTGACAAATGTGGGTGTGTGGGGCAAAAGCACT 2386
706 ThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIle 725
2387 GCCTGTAGAAAGATCTCGGTTCTTTTCCACCCCTTTCAGTTATGGCTACAATGACATGTC 2446
726 ThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArg 745
2447 ACCATCCAGCTGTGGTGCACAAACATTGATGTGAACAGGGAGTCAACCCAGGGTTCAG 2506
746 AsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAsp 765
2507 AACGACGCGAGCTACCTGGCGCTGAAGACAGCAATATGGGAGTACCTGTCTCAATGTAAC 2566
766 TyrThrLeuSerThrLeuGluGlnAspIleLysGlyValValValValValValValVal 785
2567 CTGGCCATCTCTGCCATAGACAGACATCTGTGTGAAGGGAGCCATCTGTAAGTACAGT 2626
786 GlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThr 805
2627 GGTCTCCATGCTACCTCGAGGCGCTGCAGAGCTTCCAGGCCCTCCCTGAGCCTCTTACA 2686
806 IleGlnValLeuThrVal---GlyAsnAlaLeuArgProLysIleLysTyrThrTyrPhe 824
2687 GTACAGCTCTGACTGT 2746
825 Val-----LysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 834
2747 GTTCCCATGACATGAGCTTCCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2806
835 IleProThrPhe-----SerAlaTrpValIleGluGluTrpGlyGluCysSerLysSer 852
2807 ATTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2866
853 CysGluLeuGlyTrpGlnArgLeuValGluCysArgAspIleAsnGlyGlnProAla 872
2867 TCCAGAGTACTGGCAGCGGAGCTGTGAATGCGAGGACCCCTCAGGTACAGCCTCT 2926
873 SerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892
2927 GACACCTGTGATGAGGCTCTGAAACCTGAGGATGCCAAGCCCTGTGGAGCCAGCGTGT 2986
893 Pro-----GlnTrp-----GlnLeuGlyGluTrpSerSer 902
2987 CCCTCTGATCCCTTGTGGAAATCTTATAGCTTATGGAATTTGGGCTACTGG----- 3040
903 CysSerLys 905
3041 TGTAAACAGA 3049

RESULT 8

US-09-392-184-7/c

Sequence 7, Application US/09392184

Patent No. 6395889

GENERAL INFORMATION:

APPLICANT: Robison, Keith E

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: PROTEASE HOMOLOGS

FILE REFERENCE: 5800-55

CURRENT APPLICATION NUMBER: US/09/392,184

CURRENT FILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 7

LENGTH: 3126

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(3126)

OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)

US-09-392-184-7

Alignment Scores:

Pred. No.:	6,428-191	Length:	3126
Score:	2176.50	Matches:	445
Percent Similarity:	62.46%	Conservative:	139
Best local Similarity:	47.59%	Mismatches:	243
Query Match:	41.94%	Indels:	110
DB:	4	Gaps:	23

US-09-373-658c-2 (1-950) x US-09-392-184-7 (1-3126)

Qy	59	LeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPhe	78
Db	3116	CTCACCTGTCCGCTTCGGCAAGGCTTCGRGCTGCGCTGGCGCCGACACAGCTTC	3057
Qy	79	LeuAlaProGlyPheThrLeuGlnVal-----GlyArgLysSerGlySerGlu	95
Db	3056	CTGGCGCCGACTTCAAGATCGAGCGCTCGGGGGCTCCGGCGCGGCGACCGGGGGC---	3000
Qy	96	ThrProLeuProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAsp	115
Db	2999	-----GAGCGGGGCTGGCGGCTGCTTCTTCGGCACCGTCCACGGCTCC	2952
Qy	116	ProSerSerAlaAlaLeuSerLeuGlyGlyValArgGlyAlaPheTyrLeuLeu	135
Db	2951	GCCGAGTCGCTGGCGGCGCTGAGCTGTGCCGCGGCTGAGCGGCTCTCTCTGTCGAC	2892
Qy	136	GlyGluAlaTyrPheIleGlnProLeuProAlaAlaSer-----GluArg	150
Db	2831	GGCGAGGAGTTCACATCCAGCGCGAGCGCGGGGGCTCTCTGGTTCAGCGCGACCGC	2832
Qy	151	LeuAlaThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArg	170
Db	2831	CTGCAGCGCTCGGGTCCGCG-CGAGCGCGCGCCCTCC-----CGC	2791
Qy	171	ArgAsnArgGlnGlyAspValGlyThrCysGlyValValAspAspGluProArgPro	190
Db	2790	AGGACCGAGTGGAGGTGGAGACGGAGA---GGTTCAGAGGAGGAGGAGGAGACCA	2734
Qy	191	ThrGly-LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyPr	210
Db	2733	CCAGGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2674
Qy	210	oGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyLys	230
Db	2673	A-----CCGCCCCCTGGGGGCGCCAG	2653
Qy	230	rIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAs	250
Db	2652	T---AGGACCAAGCGTGTGTCTGAGCGCGCTTCGTGGAGACGCTGCTGTGGCGGA	2596
Qy	250	pGlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSe	270
Db	2595	TGCGTCCATGCTGCTCTTACGGGGCGGACCTCGAAGAACACATCTCGAGCTTAATGTC	2536
Qy	270	rValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValVa	290
Db	2535	TGTGGAGCCCGAATCTACAGCACCACCGAGATCAAGAAATTCATCAACCTGATGTGGT	2476
Qy	290	lLysLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLe	310
Db	2475	AAAAAGTGTGATCGTAGAAGATGAAATGGGGGCCAGAGGTGCCAGCAATGGGGGCT	2416
Qy	310	uThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAl	330
Db	2415	TACACTGGTAACCTCTGCAACTGGCAGCGCGTTTCAACAGCGCCCGGACCGCCACCC	2356
Qy	330	aGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGln---Th	349
Db	2355	AGAGCACTTACGACGCGCATCTCTGCTCACCAGACAGAACTTCTGTGGGAGGAGGGGCT	2296
Qy	349	rCysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSe	369

Db	2295	GTGTGACACCCCTGGGTGTGGCAGACATCGGGAGCAATTTGTGACCCCAACAAAGCTGCT	2236
Qy	369	rValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisVa	389
Db	2235	CGTGATCGAGATGAGGGGTTCAGGGCGGCCACACCCCTGCCCATGAACCTAGGCGACGT	2176
Qy	389	lPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAs	409
Db	2175	CTCAGCATGCCCCACGACGACTCCAAGCCCTGCACACGGCTCTTCTGGGGCCATGGGCAA	2116
Qy	409	pSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCy	429
Db	2115	GCACCATGTGATGACACCGCTGTTCGTCACCTGAACACGACGCTGCTGCTGCTGCTG	2056
Qy	429	sSerAlaTyrMetIleThrSerPheLeuAspAsnGlyHis-----G1	443
Db	2055	CAGCGCATGTATCTTCACAGAGCTTCTTGACGGGGGACCGATTTTCAGGTATTTATGGC	1996
Qy	443	YgluCysLeu-MetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyT	463
Db	1995	CTGTGTCTAGGTG-----	1982
Qy	463	hrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysP	483
Db	1981	-----CTACACGCTTGCATTATGCTCTTGGGCGCGATTTCCGCCACTGCC	1936
Qy	483	roAsp-----AlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGly	501
Db	1935	CCACACCTCTGCTCAGGACGCTCTGCGCCGAGTTTGTGTC-----CACACTGATGGGCTG	1879
Qy	501	allLeuValCysGlnThrLysHis-----PheProTrpAlaAspGlyThrSerCysGlyG	519
Db	1878	AGCCCTGTGCCACACAGAAATGGCAGCTGCTGCGGCTGACGCGACCGCTGCGGGC	1819
Qy	519	lucGlyLysTrpCysIleAsnGlyLys-CysValAsnLysThrAspArgLysHisPheAsp	538
Db	1818	CTGGCACCTCTCTCAGAGGCAAGCTGCTACCTGAGGAGGAGTGGAGAGGCCCAAG	1759
Qy	539	ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCys	558
Db	1758	CCCGTGTAGATGGAGCTGGGCGACCTGGGGACCTCTGGGAGAAATGTTCTCGGACCTGT	1699
Qy	559	GlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGly	578
Db	1698	GGAGGAGGAGTACAGTTTTTCACACCGGTGATGCAAGGACCCCGAGCTTCAGAAATGAGGA	1639
Qy	579	LysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAsp	598
Db	1638	AGATCTGCTGGTTCGGAGAGCCAGTACCATGTCATGCCACGAGGAAATGCCCCCT	1579
Qy	599	AsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAla	618
Db	1578	---GACCGGAAAAAGCTTCAGGGAGCAGCTGTGAGAAATATAATGCTTACAAATTACACT	1522
Qy	619	SerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLys	638
Db	1521	GACATG---GACGGGAATCTCTGTCAGTGGTCCCCCAAGTATGCTGGGGTGTCCCGCG	1465
Qy	639	AspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnPro	658
Db	1464	GACCGTGCAGGTGTGTTCTGCGGAGCCCGGGGAGGAGGAGTTCAAAGTGTTCGAGGCC	1405
Qy	659	LysValValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGln	678
Db	1404	AGGTGATTTGATGGCACCTGTGTGGGCCAGAAAGACTGGCCATCTGTGTCTGTCGCCAG	1345
Qy	679	CysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGly	698
Db	1344	TGTTCAAGCCCGCTGTGACCATGTGTGTGACTCGCTCGGAGAGTGGACAAATCGCGG	1285
Qy	699	ValCysGlyGlyAsnGlySerThrCysLysLysLysIleSerGlySerValThrSerAlaLys	718
Db	1284	GTGTGTGGGGGCAAGGCAACTCTCTCGAGGAAGGTCTCTCGGGTCTCTACCCCAACCAAT	1225

1213	GTGATCTCTGGGTCAGGCGAGAGGGGGCCCCAAGTGGGGGCCAAGTGTGTGCCACACCCCTG	1272
Qy	ArgAsnPhcCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHis	332
Db		
1273	CGCAGCTTCTGTGCTGGCAGCGGGGCCTCAACCCCTGAGGACTCGGACCTGTACCAC	1332
Qy	TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr	352
Db		
1333	TTTGACACAGCCATCTCTGTTTACCGCTGAGGACCTGTGTGGAGTCTCCACTTGGCAGACG	1392
Qy	LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu	372
Db		
1393	CTGGGTATGGCTGATGTGGGCACCGCTCTGTGACCGCGCTCGGACCTGTGCCATTGTGGAG	1452
Qy	AspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMet	392
Db		
1453	GATGATGGCTCCAGTCAGCTCAGCCCTCACTGCTGCTCATGAATGGGTCTATGCTTTCAACATG	1512
Qy	ProHisAspAspAlaLysGlnCysAlaSerLeuAsnGly--ValAsnGlnAspSerHis	411
Db		
1513	CTCCATGACAACTCAGGCCATGATCAGATTGATGGGCTTTTGAGCACTCTCGCCAT	1572
Qy	MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAla	431
Db		
1573	GTCAATGGCCCTGTGATGGCTCAATGTGATGCTCCTGAGGAGCCCTGGTCCCCCTGCAGTGCC	1632
Qy	TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln	451
Db		
1633	CGCTTCATCACTGACTTCTCTGGACAATGGCTATGGGCACCTGTCTCTTAGACAACACAGAG	1692
Qy	AsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCys	471
Db		
1693	GCTCCATTGCACTCTGCTGTGACTTTCTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCC	1752
Qy	GlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThr	491
Db		
1753	CAGTCGACCTTGGGCCCCGACTACAGCCATTGCTCCACAGCTGCGCGCGCCCTGTGTGCC	1812
Qy	LeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrp	511
Db		
1813	CTCTGTGTCTGTGGCCACTCAATATCCACAGGCTGTGGGCTCTTGGGACCACTGG	1872
Qy	AlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLys	531
Db		
1873	GCCGATGGCACACCTCTCGGGGCCCGCACAGGCTCGCATGGGTGTGCTGCTCCACATG	1932
Qy	ThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrp	551
Db		
1933	GACCAGCTCCAGGACTCATATATCCACAGGCTGTGGGCTCTTGGGACCACTGG	1992
Qy	GlyAspCysSerArgThrCysGlyGlyValGlnTrpThrMetArgGluCysAspAsn	571
Db		
1993	GGTGACTGTCTCTGGGACCTGTGGGGGTGGTGTCCAGTTCTCTCCCGAGACTGCACGAGG	2052
Qy	ProValProLysAsnGlyLysTyrcysGlyGlyLysArgValArgTyrArgSerCys	591
Db		
2053	CTGTCTCCCGGAATGTTGCAAGTACTGTGAGGGCGCGGTACCCGCTTCGCGTCTCTGC	2112
Qy	AsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAla	611
Db		
2113	AACACTGAGGACTGCCCAACTGGCTCAGCCCTCAGCTTTCGCGAGGAGCAGTGTGTGCC	2172
Qy	HisAsnGluPheSerLysAlaSerPheGlySerGlyProAla---ValGluTrpIlePro	630
Db		
2173	TACAAACCCGACCGACCTC---TTCAAGAGCTTCCAGGGGCCCATGAGCTGGGTCTCT	2229
Qy	LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle	650
Db		
2230	CGCTACACAGGCTGGCCCCCAGGACCACTGCAAACTCACCTGCCAGGCCCCGGGCACTG	2289
Qy	GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProLysPser	670
Db		
2290	GGTACTACTATGTGTGGAGCCACGGGTGTAGATGGGACCCCTGTGTCCCGGACAGC	2349

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RESULT 10
US-09-634-286A-1
; Sequence 1, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGATE DEGRADING METALLO PRO
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0

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DB	1093	ATGGCCGCATTCCACCGCTGGGGGGCTAAAGCGCTATTCTGTAAACAGTGTATGGCAGACGA	1155
QY	273	AlaArgLeuTyrLysHisProSerLleArgAsnSerValSerLeuValValLysIle	292
DB	1153	GCCAAGGCGCTTCAGACCAACCAAGCATCCGCAATCTGTGAGCTGGTGGTGA	1212
QY	293	LeuValIleHisAspGluInLysGlyProGluValThrSerAsnAlaLeuThrLeu	312
DB	1213	GTGATCTCTGGGCTCAGCGCAGGAGGGGCCCAAGTGGGGGCCCAAGTGGCTG	1272
QY	313	ArgAsnPheCysAsnTyrGlnLysGlnHisAsnProSerAspArgAspAlaGluHis	332
DB	1273	CGCAGCTTCGTGCTCGCAGCGAGGGGGCTCAACACCCCTGAGACTCGGACCT	1332
QY	333	TyrAspThrAlaIleLeuPheThrArgInAspLeuCysGlySerGlnThrCysAspThr	352
DB	1333	TTTGACACAGCCATCTGTGTTTACCGTCAGGACCTGTGTGGAGTCTCCACTT	1392
QY	353	LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu	372
DB	1393	CTGGGTATGGCTGATGTGGGCACCGTCTGTGACCCCGCTCGGAGCTGTGCAT	1452
QY	373	AspAspGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisValPheAsnMet	392
DB	1453	GATGATGGGCTCCAGTCAGCTTCACTGTCTGCTCATGAACATGGGTCTATGCTT	1512
QY	393	ProHisAspAlaLysGlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHis	411
DB	1513	CTCCATGACAACTCCAAAGCCATCCATCAGTTTGAATGGGCGCTTTGAGCACC	1572
QY	412	MetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTyrSerProCysSerAla	431
DB	1573	GTCAATGGCCCTCTGTATGGCTCATGTGGATCTCTGAGGAGCCCTGGTCCCT	1632
QY	432	TyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGln	451
DB	1633	CGCTTCATCACTCACTTCTCTGGCAATATGGCTATGGGCACCTGTCTTTAGACA	1692
QY	452	AsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCys	471
DB	1693	GCCTCATTCGATCTGCTGTGACTTCCCTGTGCACAGCATATGATGCTGACGCC	1752
QY	472	GlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThr	491
DB	1753	CAGCTGACCTTGGGGCCGCACTCACGCCATGTGTCCACAGCTGCGCGCGCGCTG	1812
QY	492	LeuTyrCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTyr	511
DB	1813	CTCTGGTCTCTGGCCACTCAATGGCCATGCCATGTGTGCACACCAACACTCGCC	1872
QY	512	AlaAspGlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLys	531
DB	1873	GCCGATGGCACACCTTCGGGGCCCGCACAGGCTGCATGGGTGGTGCCTGCCATG	1932
QY	532	ThrAspArgLysHisPheAspThrProPheHisGlySerTyrGlyMetTyrGlyProTyr	551
DB	1933	GACCACTCCGAGCTTCAATATTCCACAGCTGTGGCTGGCTGGGGTCTTGGGAGC	1992
QY	552	GlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsn	571
DB	1993	GGTGACTGTCTCGACCTGTGGGGTGGTGTCCAGTTCTCCTCCGAGAGCTGACGAG	2052
QY	572	ProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCys	591
DB	2053	CTGTCTCCCGGAATGTGTGGCAAGTACTGTGTGAGGGCCGCGTACCGCTTCCGCT	2112
QY	592	AsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAla	611
DB	2113	AACACTGAGGACTGCGCACTGGCTCAGCCCTGACCTTCGCGAGGAGCAGTGTCTGC	2172
QY	612	HisAsnGluPheSerLysAlaSerPheGlySerGlyProAla---ValGluTyrIlePro	630
DB	2173	TACAACCAACCGCACCGACCTC---TTCAAGAGCTTCCAGGCGCCATCAGTACG	2229

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QY 631 LysTyrAlaGlyValSerProLysAspArgCysValLysLeuIleCysGlnAlaLysGlyIle 650
DB 2230 CGCTACACAGGCGTGGCCCGCCAGGACCACTGCAAACTCACTGCGAGCCCGGCACTG 2289
QY 651 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 670
DB 2290 GGTACTACTATGTGCTGGAGCCAGCGGGTGGTAGATGGGACCCCTGTTCCTCCGACAGC 2349
QY 671 ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleLeuAspSer 690
DB 2350 TCCTCGGTCTGTTCAGGCGCGATGCATCCATGCTGGCTGTGATCGCATCATTTGGCTCC 2409
QY 691 LysLysLysPheAspLysCysGlyValCysGlyValAsnGlySerThrCysLysLysIle 710
DB 2410 AAGAAGAAATTTGACAAAGTGCATGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2469
QY 711 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 730
DB 2470 TCAGGCTCTCTCAGGAATTCAGGTACGATACAAATGTGTTGCTCACTATCCCGCGGG 2529
QY 731 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 750
DB 2530 GCCACCCACATTTGTTCGGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2583
QY 751 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 770
DB 2584 TTGGCCCTCGAAGCTCCAGATGGCTCTATGCCCTCAATGTGTGATATACACCTGTATGCC 2643
QY 771 LeuGluGlnAspIleMetTyrLysGlyValVal---LeuArgTyrSerGlySerSerAla 789
DB 2644 TCCCCACAGATGTGGTACTGCTGGGACATGCTAGCTTGGCTAGCAGCGGGCCACTGCA 2703
QY 790 AlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeu 809
DB 2704 GCCTCAGAGACATGTCTAGGCGCATGGGCACTGGCCAGCTTGTGACACTGCAAGTCTTA 2763
QY 810 ThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLys 829
DB 2764 GTGCTGGCAACCCCGGACACAGCTCCGATACAGCTTCTTCGTGCCCGCCGAC 2823
QY 830 GluSerPheAsnAlaIleProThrPheSerAlaTrpVal-IleGluGlu-----Tr 846
DB 2824 CTTTCA---ACGCCACGCGCCCACTCCCGAGGACTGGTGACACGAGACAGACATTCG 2880
QY 846 p-----GlyGluCysSer----- 850
DB 2881 GAGATCCTTGGCGGCGCCCTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
QY 951 -----LysSerCysGluLeuGlyTrpGlnArg-----LeuValG 863
DB 2941 TTCTGGGCGACCGGCGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTTCTGTGTGCTC 3000
QY 863 uCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSe 883
DB 3001 ATGCTAAGACTCAGTGGGAGG-----GGCTGTGGGCGTGAGACCTGCCCTCCTC 3051
QY 883 rThrArgProCysAlaAspHisProCysPro-----GlnTrpGln-----LeuG 898
DB 3052 TCTGCCCTATGGCAGCGCTGCCCTGCCCTGGTTCTCTCCCTGGGAGGACATGTGG 3111
QY 898 yGluTrp-----SerSerCysSe 904
DB 3112 TTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3171
QY 904 rLysThrCysGlyLysGlyTyrLysLysArgSer 915
DB 3172 GGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3205
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RESULT 11

US-09-122-126B-14

; Sequence 14, Application US/09122126B

; Patent No. 6451575

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GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRESAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-122-126B-14
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Alignment Scores:

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Pred. No.: 3,49e-168 Length: 3250
Score: 1931.00 Matches: 395
Percent Similarity: 54.29% Conservative: 124
Best Local Similarity: 41.32% Mismatches: 316
Query Match: 37.21% Indels: 122
DB: 4 Gaps: 17
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US-09-373-658C-2 (1-950) x US-09-122-126B-14 (1-3250)

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QY 8 ProGlySerArgSerPheGlyProValProThrLeuLeuLeuAlaAlaLeuLeu 27
DB 196 CTTGCCCGCAGATAAAGCCGGCGGCGCTCCGACT-----GCTGCA 234
QY 28 AlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeuValProGlu 47
DB 235 GCAGCGCGCCAGCCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 291
QY 48 LeuGluArgAlaProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPhe 64
DB 292 -----CCGCGCCACCCCGCAGCCCTCGCGCAGCGCGCGAGCAAGGGCGCTG 339
QY 65 AspGlnGlnLeuAsp----- 69
DB 340 GTGCAGAACATCGACCAACTCTACTCGGCGGCGGCAAGGTGGGCTACCTGCTAGCG 399
QY 70 -----LeuGluLeuArgProAspSerSerPheLeuAlaProGlyPhe 83
DB 400 GCGCGCGCGAGGTCTCTCTGGACCTGGAGCGAGATGGTGGGCGATGCTGCTGCTTC 459
QY 84 ThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGluThrAspLeu 103
DB 460 GTG-----CCGCGCAGGCGGCGGACGAGTGGCGCTGGCGCCACCGG 501
QY 104 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 123
DB 502 AGCCACTGCTTCTATCGGGCGACAGTGGACGCTAGTCCCGCTCTCTGCTGCTTTGAC 561
QY 124 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 143
DB 562 CTCTGTGGGGGTCTCGACGGCTTCTTCGGGTCAAGCAGCGCGGTACACCTTAAGCCA 621
QY 144 Leu-----ProAlaAlaSerGlu----- 149
DB 622 CTGCTCGCGGAGCCCTGGCGCGAGGAGAAAGGGCGCGGTGTACGGGATGGTCCGCA 681
QY 150 ArgLeu-AlaThrAla----- 156
DB 682 CGGATCTCGACGCTTACACCGCGAGGGCTTCAGCTTCGAGGCCCTGCGCGCGCGCC 741
QY 156 OGlyGlyLysProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAs 176
DB 742 AGCTCGGAAACCCCGCGTCCA----- 763
QY 176 pValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGluTh 196
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Db 764 -----CACCGAGGCCACGAGCATGCTCCGGCG 792
Qy 196 rGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAs 216
Db 793 C-----ACAGCAACCCGAGCGGAGCGCAGCACTGG---CCTCGCAG 831
Qy 216 pProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----GlySerIle 231
Db 832 CTCTTGACCAAGTCCGCTCTCTCGCCGCGTGGGGGCTCAGACCGCAGACGCTGGTGGCGG 891
Qy 231 eArgLysLysArgPheValSerSerHisArgTyValGluThrMetLeuValAlaAspG1 251
Db 892 -CGCGGCGCGCTCCATCTCCCGGCGCCCGCAGGTGGAGCTCTCTGCTGCTGACGC 950
Qy 251 nSerMetAlaGluPheHisGlySerGlyLeuLysHisTyLeuLeuThrLeuPheSerVa 271
Db 951 GTCCATGGCGCGGTGTATGGCGGGCGCTGACGATTACCTGTCACCTGGCCCTCCAT 1010
Qy 271 lAlaAlaArgLeuTyTrpLysHisProSerIleArgAsnSerValSerLeuValVally 291
Db 1011 CGCAATAGGCTGTACGCCATGCTAGCATCGAGAACCATCGGCTGGCGGTGGTGA 1070
Qy 291 sIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuth 311
Db 1071 GGTGGTGGTCTAGCGCACAGCAAGAGCCCTGGAAGTGGCAAGAACGCTGCCACAC 1130
Qy 311 rLeuA-rgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGl 331
Db 1131 ACTCAGAACTTTTGCAAGTGGCAGCACCAACCAACACACCTGGGAGATGACCATGAGGA 1190
Qy 331 uHisTyAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAs 351
Db 1191 GCACACGATGACGATCTCTGTTACTCGGAGGATTTATGTGGGCATCATTCATGTGA 1250
Qy 351 pThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIle 371
Db 1251 CACCTCGGGAATGGCAGACTTGGGACCATPATCTTCTCCAGCGCGAGCTGTCTGTGAT 1310
Qy 371 eGluAspAspGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisValPheAs 391
Db 1311 TGAAGACGATGGCTTCCAGCAGCTTCACTGGCTCAGCAATCGACATTTACTTGG 1370
Qy 391 nMetProHisAspAlaLysGlnCysAlaSerLeuAspGlyValAsnGlnAspSerHi 411
Db 1371 CCTCTCCATGACGATTCCAAACTCTGTGAAGAGACCTTTGGTTCCACAGATGAAGCG 1430
Qy 411 sMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAl 431
Db 1431 CTTAAATGCTTCCATCTTACCAGCATGTGATCATTAAGCCCTGGTCCAAATGCACTTC 1490
Qy 431 aTyMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProG1 451
Db 1491 AGCCACCATCACAGAATCTCTGATGATGGCCATGTTAACTGTTTGTGGACCTTACCAG 1550
Qy 451 nAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyAspAlaAsnArgGlnCy 471
Db 1551 AAAGCAGATCTCTGGGCCCCGAGAACTCCAGACAGACCTACGATGCCACCCAGCAGTG 1610
Qy 471 sGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerTh 491
Db 1611 CAACCTGACATTCGGGCTGAGTACTCCGNGTCTCC---GGCATGGATGCTGTGCTCG 1667
Qy 491 rLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrIleHisPheProTr 511
Db 1668 CTTGTGTGTGTGTGTAGCCAGGCGCCAGATGGTCTGTCTGACCAAGAGCTGCTCTGC 1727
Qy 511 pAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLy 531
Db 1728 GGTGGAAAGGACGCTTGTGAAAGGGGAAATCTGCTTCAGCGGCAATGTGTGACAA 1787
Qy 531 sThrAspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTr 551
Db 1788 AACCAAGAAAATAATTATTCAACGTCAGGCCATGGCAACTGGGGGATCTTGGGGATCCTG 1847

Qy 551 pGlyAspCysSerArgThrCysGlyGlyValGlnTyThrMetArgGluCysAspAs 571
Db 1848 GGGCCAGTGTCTCGCTCATGTGGAGGAGTGCAGTTTGCCTATCGTCACTGTATAAA 1907
Qy 571 nProValProLysAsnGlyGlyLysTyCysGluGlyLysArgValArgTyArgSerCy 591
Db 1908 CCTGTCTCCAGAAACAACGAGCGCTACTGCAAGGAAGAGGGCCATCTTACCGCTCCG 1967
Qy 591 sAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAl 611
Db 1968 CAGTCTCATGCCCTGCCACCC---AATGTTAAATCATTTCTGTCATGAACAGTGTGAGGC 2024
Qy 611 aHisIleGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProly 631
Db 2025 CAAAATAGCTCATCTGATGCAAAAGGAGTCAAAACTTTTGTGGAATGGGTTCCCAA 2084
Qy 631 sTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleG1 651
Db 2085 ATATGCAAGTGTCTGCCAGCGGATGTGTGCAAGCTGACCTGCAGAGCCAAAGGCACTGG 2144
Qy 651 yTyPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerTh 671
Db 2145 CTACTATGTGTATTCTTCTCCAAAGGTGACCGACTGAATGTAGCCCGTACAGTAA 2204
Qy 671 rSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSerLy 691
Db 2205 TTCCGTCTCGTCCGGGGAAGTGTGAGAACTGGTGTGACGGCATCATTCGCTCAA 2264
Qy 691 sLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSe 711
Db 2265 GCTGCATGATGACAAAGTGGGAGTATGTGGAGGAGACAACTCCAGCTGTACAAAGATTGT 2324
Qy 711 rGlySerValThrSerAlaLysProGlyTyRHisAspIleIleThrIleProThrGlyAl 731
Db 2325 TGAACCTTTAATAAGAAAGTAAAGGTTTACACTGACGTGGTGAGGATTCCTGAAGGGC 2384
Qy 731 aThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnGlySerPheLe 751
Db 2385 AACCCACATAAAGTTTCGACAGTTCAAAGCCAAAGACACAGACTAGATTCACTGCCTATT 2444
Qy 751 uAlaIleLysAlaAlaAspGlyThrTyIleLeuAsnGlyAspTyThrLeuSerThrIle 771
Db 2445 ACCCTGAAAGAAAGAAACGGTGTACTCTTATCAATGGAAGATCATGATCTCCACTTC 2504
Qy 771 uGluGlnAspIleMetTyLysGlyValValLeuArgTySerGlySerSerAlaAlaLe 791
Db 2505 AGAGACTCATTTGACATCAATGGAACAGTCATGAACTATACGGTGGAGCCACAGGCA 2564
Qy 791 uGluArgIleArg-----SerPheSerProLeuLysGluProLeuThrIleGlnValle 809
Db 2565 TGACTTCTGTCATGGCATGGCTACTCTGCCACGAAGAAATTCCTAATAGTGCAGATTCT 2624
Qy 809 uThrValGlyAsnAlaLeuArgProLysIleLysTyThrTyRPhVal---LysLysLy 828
Db 2625 TGCAACAGACCCCATTAACCATTAAGATGTGCGTTATAGCTTTTGTTCACAGAGTC 2684
Qy 828 sLysGluSerPheAsnAlaIleProThrPheSerAla----- 840
Db 2685 CACTCCAAAAGTAAACTCTGTCACTAGTCGCGCAGCAATAAAGTGGGATCACACACTTC 2744
Qy 841 -----TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTr 857
Db 2745 GCAGCGCAGTGGGTCACGGGCCCCATGGCTCCCTCTAGGACCTGTGACACAGGTTG 2804
Qy 857 pGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLy 877
Db 2805 GCACACCAAGACGGTGCAGTGCAGAGTGAACCGGAAGTTAGCAAAAGAGGATGCTCTCT 2864
Qy 877 sGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892
Db 2865 CTCCCAAGAGGCTTCTCGGTTAAGCAATGCTTGTGAAGAAATGT 2910

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RESULT 12
US-09-634-286A-14
; Sequence 14, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGATE DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634,286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)..(2910)
US-09-634-286A-14

Alignment Scores:
Pred. No.:      3,49e-168      Length:      3250
Score:          1931.00        Matches:      395
Percent Similarity: 54.23%     Conservative: 124
Best Local Similarity: 41.32%   Mismatches:    316
Query Match:       37.21%     Indels:       122
DB:                4           Gaps:         17

US-09-373-658C-2 (1-950) x US-09-634-286A-14 (1-3250)

QY      8 ProGlySerArgSerPheGlyProValProThrLeuLeuLeuAlaAlaLeuLeu 27
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Db      196 CCTGCCAGATAAAGCCGGCGAGCTCCGACT-----GCTGCA 234

QY      28 AlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeuValProGlu 47
      ||| :||
Db      235 GCAGCGCGCCACGCCCGCGCGGCGAGGGGAGGTGCAGGAGTCAGCCGAGCT-- 291

QY      48 LeuGluuArgAlaProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPhe 64
      |||||
Db      292 -----CCGGGCAACCCGACCCCCCTGCGCGAGCGCGGAGGAGGAGGGGTG 339

QY      65 AspGlnGlnLeuAsp-----
      ||| :||
Db      340 GTGCAGAACATCGACCAACTCTACTCCGGCGCGGCAAGGTGGGCTACCTCGTTACGGC 399

QY      70 -----LeuGluLeuArgProAspSerSerPheLeuAlaProGlyPhe 83
      |||||
Db      400 GCGCGCGGAGGTTCTCTTTCGACCTTGAGCGGAGATGTTGGTGGGCATTGCTGGCTTC 459

QY      84 ThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGluThrAspLeu 103
      ||| :||
Db      460 GTG-----CCGCGAGAGGCGGACGAGTGGCCCTGGCGCCACCAG 501

QY      104 AlaHisCysPheTyrrSerGlyThrValAsnClyAspProSerSerAlaAlaLeuSer 123
      :|||
Db      502 AGCCACTGCTCTATCGGGGACAGTAGTGACGCTAGTCCC CGCTCTCTGGCTGTCTTTGAC 561

QY      124 LeuCysGluGlyValArgGlyAlaPheTyrrLeuLeuGlyGluAlaTyrrPheIleGlnPro 143
      ||| :||
Db      562 CTCCTGGGGGTCTCGACGGCTTCTTCGCGGTCAAGCACGCGCGCTACACCTTAAGCCA 621

QY      144 Leu-----ProAlaAlaSerGlu-----
      |||
Db      622 CTGCTCGCGGAGCCCTGGCGGAGAAAGAAAAGGGGCGGTGTACGGGATGGGTCGCCGA 681

QY      150 ArgLeu-AlaThrAla-----
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Db      682 CGGATCTCGACGCTACACCCGCGAGGGCTTACGTTTCAGTTCGAGGCCCTGCGCGCGCGCTC 741

QY      156 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAs 176
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QY 153 ThrAlaAlaProGlyGluLysProProAlaProLeuGlnPheHisLeuLeuA:rgAsn 172
Db 564 -----GGGGATGGATCTTCCCGCATCTGTCATCTCTAC : : : : :
QY 173 ArgGlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGly 192
Db 600 GCGAGGSC-----TTTAGCTTCAGGCCCTGCGCCA--- 632
QY 193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp 212
Db 633 CGCGCCAGTTGCGAG-----ACTCTGCATCCCCATCTTGGGCCCAAGAG 677
QY 213 SerProGln-----AspProAlaLeu----- 219
Db 678 AGCCCTCGGTGCACAGTAGATCTAGAGAGCGTCAAGCGTCCCGCCGAGCTGCTGGAC 737
QY 220 GlnGlyValGlyGlnProThrGly-----ThrGlySerIleArgLysLys 234
Db 738 CACTCAGCTTCTCGGCATCTGGCAACGCGGAGCTCAGACTTGGTGGAGCGTAGGCGC 797
QY 235 ArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAla 254
Db 798 CGTTCATCTCCAGGCGCCCGAGGTGGAGCTCTCTGTGGTCTGACTCGTCCATGGCC 857
QY 255 GluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArg 274
Db 858 AGGATGATGGGCGGCGCTGCAGCATTAACCTGTCACCATGCGCTCCATGCCAACAGS 917
QY 275 LeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeuVal 294
Db 918 CTGTACAGTCATCAAGCATGTAGAACACCATCCGCTGGCGGTGGTGAAGGTGGTGGT 977
QY 295 IleHisAspGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsn 314
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QY 315 PheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAsp 334
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QY 335 ThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGly 354
Db 1098 GCAGCCATCTGTTCACCGAGAGGATTTATGTGGCATCATTCATGTGACACCTTGGGA 1157
QY 355 MetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAsp 374
Db 1158 ATGGCAGAGCTTGGGACCATATGTTCTCGGAGCGCAGCTGTGCACTGATTGAAGATGAT 1217
QY 375 GlyLeuGlnAlaAlaPheThrAlaHisGlyLeuGlyHisValPheAsnMetProHis 394
Db 1218 GGCTTCATCGACCTTCACTGGCTCATGAATTTGGGCATCTACTTGGCCTTTCTCAT 1277
QY 395 AspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAla 414
Db 1278 GACGATTCCAAAATCTGTGAAGAGAACTTCGGTACTACAGAGACAAAGCGTTATGTCT 1337
QY 415 SerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMetIle 434
Db 1338 TCAATCTTACGACATCATCATCCAGCCCTGGTCCAAATGCAAGTCAGCGTCAACCCATC 1397
QY 435 ThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIle 454
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QY 455 GlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThr 474
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QY 495 ThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAspGly 514

Db 1575 GCTGTGTGTCGCGCAAGGCCAAATGCTGTCTGCACCAAGAGCTGCGGCTGTGGAGGSC 1634
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Db 1635 ACTCCTGTGGGAAGGAGAGTCTGCCCTTCAAGGCAATGTGTGACAAAATAAGAAA 1694
QY 535 LysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCys 554
Db 1695 AAATATTACTGCATCAAGCCATCAAGAAATGGGGTCTCTGGGGCCCTCTGGGTCAGTGT 1754
QY 555 SerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValPro 574
Db 1755 TCTCCTCATGCGGGGAGGAGTGCAGTTTGCTTACCCTCATTTGTAATAACCTGCACCT 1814
QY 575 LysAsnGlyGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGlu 594
Db 1815 CGAAACAGTGGCGCTACTGCACAGAGAGGCGCCATATACCGTTCTCTCAGTGTTACA 1874
QY 595 AspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGlu 614
Db 1875 CCCTCCCAACCC---AATGGTAAATCTTTTCCGCTAGCAGTGTGAAGCCAAAATGSC 1931
QY 615 PheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGly 634
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QY 635 ValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePhe 654
Db 1992 GTCTCTGCGCGGAGATGTGTGCAAGCTTACTCTGCAGAGCTAAGGCGACAGGCTACTATG 2051
QY 655 ValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCys 674
Db 2052 GTCTTTTCTCCNAAGTTTACGATGGAGTGAATGACGCGGTACAGCACTCTGTGTGT 2111
QY 675 ValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysPhe 694
Db 2112 GTCCGAGGACGCTGTGTGAGAACTGATGTGACGCAATTATTGGCTCAAAGTCAATAT 2171
QY 695 AspLysCysGlyValCysGlyLysAsnGlySerThrCysLysLysLysLysSerVal 714
Db 2172 GACAAGTGTGAGTGTGCGAGGGGATACTCCAGTTGTACAAAGATTATCGGAACCTTC 2231
QY 715 ThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyValAlaThrAsnIle 734
Db 2232 AATAAAAAAGCAAGGTTTACTGACGTTGTGAGGATCCCTGAAGAGCAACCCACATA 2291
QY 735 GluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaLys 754
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QY 813 AsnAlaLeuArgProLysIleLysTyrThrTyrPheVal---LysLysLysLysGluSer 831
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QY 832 PheAsnAlaIle-----ProThrPheSerAla 840
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Qy 881 ProAlaSerThrArgProCysAlaAspHisProCys---ProGlnTrpGlnLeuGlyGlu 899
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Db 2820 TACTCTAA-TGCACAAAAAACACAGGAGGATCATGCCAGATACAGCTGTGGTGAAGAC 2878
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RESULT 14
US-09-369-364A-12
; Sequence 12, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurstainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5804
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(5648)
; NAME/KEY: misc feature
; LOCATION: (1406)
; OTHER INFORMATION: n-T
; NAME/KEY: misc feature
; LOCATION: (1563)
; OTHER INFORMATION: n-T
US-09-369-364A-12
Alignment Scores:
Pred. No.: 1,26e-151 Length: 5804
Score: 1756.50
Percent Similarity: 50.93%
Best Local Similarity: 36.11%
Query Match: 33.85%
Indels: 193
Gaps: 24
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Qy 80 AlaProGlyPheThrLeuGlnAenValGlyArgLysSerGlySerGluThrProLeu--- 98
Db 369 GCTCCACTGTCTACTGTCACTCTCTGGGACGCCCGGGGTGAATCAGACCAAGTTTAT 428
Qy 99 -----ProGlnThrAspLeuAlaHisCysPheTyr-SerGlyThrValAsnGlyAspPr 116
Db 429 TCCGAGAGACGGCGGAACCTAAGACACTGTCTTACAAAGGGTATGTATACCAACTC 488
Qy 116 oSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuG1 136
Db 489 CGAGCACACGGCGGTCTATGCTCTGCTCAGGAATG----- 525

Qy 136 yGluAlaTyrPheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaPr 156
Db 526 -----AACACAAAATAGGCACAGTAAGAC 551
Qy 156 oGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAs 176
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Qy 195 uThrGluAspGluAspGluGlyThrGluGlyGluAspGlyGlyProGlnTrpSerProG1 215
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Db 696 -----AGGCAAAACG 706
Qy 235 gPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaG1 255
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Db 827 CTATAAAGACCCAGATTTTGAATTAATTAATTAATTTATTTGTGAATTAATTTGAT 886
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Db 887 TCATAATGAACAGGATGGGCTTCCATATCTTTAATGTCTCAGACAACTAAATAAATTT 946
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Db 947 TTGCCAGTGGCAGCATTCGACAGTCCA-----GGTGGATCATCATGATAC 994
Qy 335 rAlaIleLeuPheThrArgGlnAspLeuCys---GlySerGlnThrCysAspThrLeuG1 954
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Qy 354 yMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAs 374
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Db 1115 TGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCCATGTGTTTAACTGCTCA 1174
Qy 394 sAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAl 414
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Qy 434 eThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn---Pr 453
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Qy 453 oIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPh 473
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Db 1469 GTGCAATTAACGTCATGAGTACACAAAGGCTCGCGACTCAGCACACACCTTGGCCGA 1528
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Db 1529 TGGACGGAGTGGAGCTGGGAAGCACTGCAAGNATGATTTGTGTT 1577
Qy 533 pArgLysHisPheAspThrProPhe---HisGlySerTrpGlyWetTrpGlyProTrpAl 552
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Qy 572 oValProLysAsnGlyLysThrCysGlyGlyLysArgValArgTyrArgSerCysAs 592
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Qy 592 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHi 612
Db 1757 CACGGAGCCATGTCACAGCAGAAAG---CGAGACTTCCGAGATGAACAGTGT---GCTCA 1810
Qy 612 sAsnGluPheSerLysAlaSerPhe-----GlySerGlyProAlaValGluTrpIl 629
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Qy 629 eProLysTrpAlaGlyLysSerProLysAspArgCysLysLeuLysCysGlnAlaLysGl 649
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Qy 649 yLeuGlyThrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAs 669
Db 1925 GAACACAGCTTACTACGTTCGAGAGCAGAGTGAATGATGAGTGAATCTCTTGTGGCCAGGA 1984
Qy 669 pSerThrSerValCysValGlnGlyLysValLysAlaGlyCysAspArgGlyLeuAs 689
Db 1985 CACAATGATATCTGTGTGTCAGGGCTTTGCGGCAAGCTGGATGCGATCATGTTTAA 2044
Qy 689 pSerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLy 709
Db 2045 CTCAAAACCCGGAGAGATAATGCGGGGTTTGTGTGGCGATAATCTTTCATGCAAAAC 2104
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Qy 749 rPheLeuAlaLysAlaLysAlaAspGlyThrTyrLysLeuAsnGlyAspTyrThrLeuSe 769
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Qy 769 rThrLeuGluGlnAspLeuMetTyrLysGlyValValLeuArgTyrSerGlySerSerAl 789
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Db 2405 GTGCGTGGGAAGTTGTACAAACCCGATGATGCGTATTCCTTCAATATTCATTTGAGA 2464
Qy 825 -----825
Db 2465 TAAACCTCAGCAGTTTTTACTGGAACAGTATGCGGCCATGCGAAGCATGCGATTAACCCCTG 2524
Qy 826 -----LysLysLys-----LysGluSer-----831

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Qy 831 -----831
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Qy 831 -----831
Db 2645 CTGTGACCTGAGTGGCAGTGTGCCAGCAGGAGTGAATGTAGTGCCTCCAGTGTGCTTGG 2704
Qy 832 -PheAsnAlaLysProThrPheSerAla-----840
Db 2705 TTACCGCATTGGACATCTACTGTGCCAAATATAGCAGGCTGGATGGGAACACTGAGAA 2764
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Db 2765 GCTTGTATGATGTTTGTGACGACGACCATCCCAAAACCAAGCAACCTGAAAAATGCTCAGG 2824
Qy 841 -----TtpValLleGluGluTrpGlyGluCysSerLysSerCysGly 854
Db 2825 GGAATGTAAACAGCGGTGGCTGCGCTATTCTGCTGAGCTGAAAGTTTCAAAAGCTGTGA 2884
Qy 854 uLeuGlyTrpGlnArgArgLeuValGluCysArgAspLeuAsnGlyGln-----ProAl 872
Db 2885 CGGTGGACCCAGAGGAGAGGGCTATTGTGTCAATACCCGAAATGATGTACTGGATGA 2944
Qy 872 aSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCy 892
Db 2945 CAGCAATGTACACATCAGAGAAAGTTCACATTACAGAGG---TGCAGTGAAGTCCCTTTG 3001
Qy 892 sProGlnTrpGlnLeuGlyLysSerSerCysSerLysThrCysGlyLysGlyTyrLy 912
Db 3002 TCCACAGTGAATCTGGAGACTGGTCAGAGTGTCTGGTCACTGTGGAAAAGGCGATAA 3061
Qy 912 sLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAs 932
Db 3062 GCACAGCCAGTCTGGTGTGCTGAGTGTGAGAGTGAATGGAATGATGATGATGGA 3118
Qy 932 pProLeuLysLysProLysHisPheLeuAspPheCysThrMetAlaGluCysSer 950
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; Sequence 14, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Mus musculus ADAMS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2) (2623)
US-09-369-364A-14

Alignment Scores:
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Score: 1611.00 Matches: 340
Percent Similarity: 55.99% Conservative: 146
Best Local Similarity: 39.17% Mismatches: 312
Query Match: 31.05% Indels: 71
DB: 4 Gaps: 26

US-09-373-658C-2 (1-950) x US-09-369-364A-14 (1-2625)

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Db 68 TTCATTGAACCACTCGAGTCTGGATGAGCAA ---GAGGATGAAGAGGAA 115
Qy 160 ProProAlaProLeuGlnPheHisLeuLeuArgAlaAsn ---ArgGlnGly 175
Db 116 CAAAACAAACCC ---CACATTATTATAGCCACAGCACCCCTCAGAGGACCC 166
Qy 176 AspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGlu 195
Db 167 TCCACAGAAAGACATGCTGTGCCACTCAGAACTCAAAATAGTCACAGTAAAGA-CAA 225
Qy 196 ThrGluAspGluAspGluGlyThrGluGlyGluAsp --- 207
Db 226 CGGGAATCAGATGCCAAACGAGAAAGAGGAATAGCTCGCTGACGAGCTGGCACT 285
Qy 208 ---GluclyProGlnTTPSerProGlnAspProAlaLeuGln 220
Db 286 GCTAAAGACGGTTTGGCAACAAAGAGTGCTCTCGTCTATAGCAA--CCAGACAAACAA 342
Qy 221 GlyValGlyGlnProThrGlyThr-GlySerIleArgLysLysArgPheValSerSerHi 240
Db 343 CACAAGGGACAG-----ATGGAACCAACAAAGAACCAAAACGCTTTCTGCTCATCCC 393
Qy 240 sArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGl 260
Db 394 ACGGTTTGTAGAGGTGATGGTGGCTGACCACAGGATGGTTTTATACCACGAGCAAA 453
Qy 260 yLeuLysHisTyrLeuThrLeuPheSerValAlaAlaArgLeuTyLysHisProSe 280
Db 454 CCTTCAACATTATATCTTAACCTTAATGTCCATTCTAGCTCTCTATCTATAAGACTCAAG 513
Qy 280 rIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300
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Qy 300 sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTPrGlnLys 320
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Qy 399 nCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAs 419
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Qy 439 pAsnGlyHisGlyGluCysLeuMetAspLysPro---GlnAsnProIleGlnLeuProGl 458
Db 982 CACTGGGTACGAGAGTGCTTGTGAATGAACCTGCACTCAGGACCTATCTCTTGGCTTC 1041

Qy	458	yAspIeuPProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAs	478
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Qy	518	yGluGlyLysTipCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAs	538
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Qy	538	pThrPro---PheHisGlySerTipGlyMetTipGlyProTipGlyAspCysSerArgTh	557
Db	1267	GGGCGCTTGCAAATTGATGCATCTGGGAGGTGTGAGCCACTTTTGGGACCTGCTCAAGAAC	1326
Qy	557	rCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGl	577
Db	1327	GTGTGGAGGAGCATCAAAACAGCCATCAGAGAGTGCACAGACCAGAGCCAAAATGG	1386
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Db	1387	TGGGAAGTACTGTGTAGGAAGGAAATGAAAGTTTCAATCTCTGCAACAACCGAGCCCTGCAT	1446
Qy	597	oAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLy	617
Db	1447	GAAGCAGAAG--CGAGACTTCCGAGGAGGAGCAGTGT--GCTCAC-----TTTGATGG	1494
Qy	617	sAlaSerPhe-----GlySerGlyProAlaValGluTipIleProLysTyrAlaGl	634
Db	1495	CAAAACACTTCAACATCAATGCTGTGTCGCCACCGCTACGCTGTGTTCTTAAGTACAGCGG	1554
Qy	634	yValSerProLysAspArgCysLysLeuIleCysGlcAlaLysGlyIleGlyTyrPhePh	654
Db	1555	AATTTTGCATGAAGACCGGTGCAAGTTGTTCTCCAGAGTGGCAGGAACAACACGCTACTA	1614
Qy	654	eValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCy	674
Db	1615	CCAGCTCCGAGCAGAGTGAATTCAGGAACCCCTTGTGCCAGGACACAAATGACATCTG	1674
Qy	674	sValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPh	694
Db	1675	TGTCCAAGGCTTTGCCGCAAGCTGATGATCATATTTAAACTCAAAGCTCCGAA	1734
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Db	1735	AGATAATGTGGATTTGTGGTGGAGATAATCTTCATGCAAAACAGTGGCAGGAACATT	1794
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Db	1795	TAAACATGCTCAATTATGTTTACAATACTGTGTGTCGAATTTCCGGCTGGTGCTACCAAGAT	1854
Qy	734	eGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLy	754
Db	1855	TGACGTGCGTCAACAGCTTCTCAGGAAGTCTGAGGATGACAACTACTACGTATTATC	1914
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Db	1915	AAACAGATAAAGTGAATTCCTGTAATGGAGACTTTGTGTCTCCATGTCCAAAAGGA	1974
Qy	774	pIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIl	794
Db	1975	GGTCCCGTGGGAGCGCCGTCTATGATACAGCATCGGCAATGTGTGTGAAGACT	2034
Qy	794	eArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAl	814
Db	2035	GAACTGTACGGACCGTATCAGAGAACTTCTCTCTCAGGTGTGTCCGTGGGAAGCT	2094

QY	814	aLeuArgProLysIleLysTyrThrTyrPhe-----ValLysLysLysLysLysGluSerPh	832
Db	2095	GTATAACCCAGATGTCGGTACTCAATTCATATTCCTGAGGACAAACCTCAGCAATT	2154
QY	832	eAsnAlaIleProThrPheSerAlaTTPValIleGlu---GluTTPGlyGluCysSerily	851
Db	2155	T-----TACTGGAACAGTCACGGCGCGTGGCAAGCATGCAGCAA	2193
QY	851	sSerCysGluLeuGlyTTPGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnPr	871
Db	2194	GCCCTGCCAAGGGGAGCGGAGACCAAACTTGTGTGCACCGAGTCTGTATCAGCTAAC	2253
QY	871	oAlaSerGlu-----CysAlaLysGluValLysProAlaSer---ThrArgProCysAl	888
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QY	888	aAspHisProCysProGlnTTPGlnLeuGlyGluTTPSerSerCysSerLysThrCysG1	908
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QY	908	YlysGlyTyrLysLysArgSerLeuLysCysLeuSerHis-----AspGlyGlyVa	925
Db	2374	TTTGGCTACCGTACTTTAGACATCCACTGTGCCAAATACAGCAGGATGCGGGAAGAC	2433
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Search completed: June 18, 2004, 19:00:01
Job time : 286.679 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 18:42:30 ; Search time 931.168 Seconds

(without alignments)

4673.735 Million cell updates/sec

Title: US-09-373-658C-2

Perfect score: 5189

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09373658/runat_18062004_135345_10353/app_query.fasta_1.2254

-DB=Published Applications NA -QFMT=fastap -SUFTX=rnpb -MINMATCH=0.1

-LCOOPL=0 -LCOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct-THR_MAX=100

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Database :

Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	5189	100.0	4014	15	US-10-113-286-1	Sequence 1, Appli
4	5189	100.0	4676	14	US-10-105-929-1	Sequence 57, Appli
5	5181	99.8	4309	15	US-10-210-120-57	Sequence 192, App
6	5181	99.8	4459	16	US-10-159-563-192	Sequence 308, App
7	5181	99.8	4459	16	US-10-159-563-308	Sequence 17, Appli
8	5181	99.8	4760	10	US-09-971-4299-17	Sequence 125, App
9	5144	99.1	4014	11	US-09-989-687-125	Sequence 26851, A
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13	4292	82.7	4878	12	US-10-152-319A-1840	Sequence 170, App
14	4292	82.7	4878	16	US-10-191-803-170	Sequence 2, Appli
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16	3947	76.1	2184	15	US-10-097-597-2	Sequence 2, Appli
17	3947	76.1	2184	15	US-10-097-580-2	Sequence 13, Appli
18	3677	70.9	2184	9	US-09-445-023A-13	Sequence 13, Appli
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23	3328	64.1	3147	9	US-09-803-589-1	Sequence 9, Appli
24	2667	51.4	3145	9	US-09-803-589-9	Sequence 27, Appli
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28	2483	47.9	2867	13	US-09-741-151-1	Sequence 24, Appli
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33	2340	45.1	3711	17	US-10-283-975A-398	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-09-373-658-1

Sequence 1, Application US/09373658

Publication No. US20030092900A1

GENERAL INFORMATION:

APPLICANT: Iruela-Arispe, Luisa

APPLICANT: Hastings, Gregg A.

APPLICANT: Ruben, Steven M.

APPLICANT: Jonak, Zdenka L.

APPLICANT: Trull, Stephen H.

APPLICANT: Fronwald, James A.

APPLICANT: Terrett, Jonathan A.

TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides

FILE REFERENCE: 1488.1070006

CURRENT APPLICATION NUMBER: US/09/373,658

CURRENT FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 145

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3261

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:


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US-09-373-658-1

Alignment Scores:
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US-09-373-658C-2 (1-950) x US-09-373-658-1 (1-3261)

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Db 781 CTAAGCATTACCTTCTCACGTTGTTTCGTCGGCAGCCAGATTGTACAACACCCCCAGC 840
Qy 281 IleArgAsnSerValSerLeuValValValLysLysLeuValLysLeuHisAspGluGlnLys 300
Db 841 ATTCTGTAATTCAGTTAGCTTGGTGGTGGTGAAGATCTTGGTCATCCACGATGAACAGAAG 900
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 901 GGGCCGGAGTGAACCTCCATGCTGCCCTCACCTCTGGGAACCTTTGCACTGGCAGAAG 960
Qy 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaAlaLeuPheThr 340
Db 961 CAGCACAAACCCACCGAGTCACCGGATGTCAGACACATATGACACAGCAATTCCTTTTCACC 1020
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1021 AGACAGACTTGTGTGGTCCAGACATGTGTACTCTTGGGATGGCTGATGTTGGAAC 1080
Qy 361 ValCysAspProSerArgSerCysSerValLysGluAspAspGlyLeuGlnAlaAlaPhe 380
Db 1081 GTGTGTGATCCGAGCAGAAAGCTGCTCGTCATAGAAGATGATGTTTACAAGCTGCCTTC 1140
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db 1141 ACCACAGCCCTGATATTAGGCCACGTTGTTAACTGTCACATGATGATGATGATGATGAT 1200
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1201 GCCAGCGCTTAATGCTGAACACAGGATTCACACATGATGCGCTCAATGCTTTCCAACTG 1260
Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db 1261 GACCACAGCAGCGCTTGGTCTCTCTCGAGTGCCTACATGATTAACATTCATCTTGGATAAT 1320
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1321 GGTTCATGGGGAATGTTTGTGATGACACAGCTCAGAAATCCCATACAGCTCCAGCGCATCTC 1380
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db 1381 CCTGGCAGCTCGTACGATGCCAACCGGCGAGTGCAGTTTACATTTTGGGGAGGACTCCAAA 1440
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
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Qy 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db 1501 GTGCTGTGTGTCAAAACCAACACTTTCGCTGGCGGATGGCAGCCAGCTGTGGAGAAGGG 1560
Qy 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
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Qy 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db 1621 TTTTCATGGAAGCTGGGGAATGTGGGGCGCTTGGGAGACTGTTTCGAGAAACGTGCGGTGA 1680
Qy 561 GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db 1681 GGAGTCCAGTACAGGATGAGGAAATGTGAACCCAGTCCCAAGAAATGAGGAGAAATAC 1740
Qy 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsn 600
Db 1741 TGTGAAGGCAACGAGTGGCTACAGATCCTGTAACTTGAAGTGTGAGACTGTCCAGACATAAT 1800

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QY 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
 DB 1801 GGAANAACCTTTAGAGAGGACAAATGGAAGCACACACAGAGTTTCAAAAGCTTCCTTT 1860
 QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
 DB 1861 GGGAGTGGCCCTCGGTGGAATGATTCACAGTACGCTGGGCTCTCACCAGGACAGG 1920
 QY 641 CysLysIleCysGlnAlaLysGlyIleGlyTyrPheValLeuGlnProLysVal 660
 DB 1921 TGCAGCTCATCGCCAGCCAAAGCATGTGTACTTCTTGTGTTGAGCCCAAGGTT 1980
 QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
 DB 1981 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGCAAGGACAGTGTGTA 2040
 QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysIlePheAspLysCysGlyValCys 700
 DB 2041 AAGCTGGTGTGATCGCATCATAGACTCCAAAGAGTTTGAATAATGTGTGTTC 2100
 QY 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
 DB 2101 GGGGGAATGGATCTACTTGTATAAATAATATCAGGATCAGTTACTAGTCAAAACCTGGA 2160
 QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
 DB 2161 TATCATGATATCATCAATTCCACTGGAGGCCACCAACATCGAAGTGAACAGCCGAAC 2220
 QY 741 GlnArgGlySerArgAsnGlnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
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 QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleValTyrLysGlyVal 780
 DB 2281 ATCTCTTAATGGTGACTACACTTTGTCCACCTTAGAGCAAGACATATATGACAAAGGTGT 2340
 QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
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 QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
 DB 2401 AAAGAGCCCTTGACCATCCAGGTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2460
 QY 821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
 DB 2461 TACACCTACTTCTGTAAGAGAGAGAGAAATCTTTCAATGCTATGCCCTTTTTCAGCA 2520
 QY 841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
 DB 2521 TGGGTCAATCAAGAGTGGGCGAATGTTCTAAGTCATGTGAATGGTTGGCAGAGAGA 2580
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 DB 2821 ATAGACTTTTGCACAATGGCAGAAATGCAGT 2850

RESULT 2

US-09-989-687-1
 : Sequence 1, Application US/09989687
 : Publication No. US20040002449A1
 : GENERAL INFORMATION:
 : APPLICANT: Hastings, Gregg A.
 : APPLICANT: Ruben, Steven M.
 : TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
 : FILE REFERENCE: 1488.107000D
 : CURRENT APPLICATION NUMBER: US/09/989,687
 : CURRENT FILING DATE: 2001-11-21
 : NUMBER OF SEQ ID NOS: 126
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 1
 : LENGTH: 3261
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (1)...(2853)
 : NAME/KEY: misc feature
 : LOCATION: (3195)
 : OTHER INFORMATION: n is any nucleic acid
 : NAME/KEY: misc feature
 : LOCATION: (3248)
 : OTHER INFORMATION: n is any nucleic acid
 : NAME/KEY: misc feature
 : LOCATION: (3255)
 : OTHER INFORMATION: n is any nucleic acid
 : NAME/KEY: misc feature
 : LOCATION: (3261)
 : OTHER INFORMATION: n is any nucleic acid
 : US-09-989-687-1
 Alignment Scores:
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 Score: 5189.00 Matches: 950
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
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 DB 1 ATGGGGAGACGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCCCTACCCAGCTGCTG 60
 QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
 DB 61 CTGCTCGCGCGCGCTACTGCGCGTGTGCGACGCACTCGGCGCGCCCTCCGAGGAGGAC 120
 QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
 DB 121 GAGGAGCTAGTGGTCCGAGCTGGAGCGCGCCCGGACACGCGACACGCGCTCCGC 180
 QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
 DB 181 CTGCAGCCCTTTGACCAGCAGCTGGATCTGGAGCTCGGCGCCGACAGCAGCTTTTGGCG 240
 QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
 DB 241 CCCGCTTCACGCTCCAGAACCTGGGGCGCAATCCGGTCCGAGACCGCGCTTCCGGAA 300
 QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120
 DB 301 ACCGACCTGGCGCACTGCTTCTACTCCGACACCGTGAATGGCGATCCACAGCTCGGCTGCC 360
 QY 121 AlaLeuSerLeuCysGlnGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
 DB 361 GCCCTCAGCTCTGGAGGGCGTGGCGCGCTTCTACCTCTGGGGAGGCGTATTTC 420
 QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160

421 ATCCAGCGCGTCCCGCGCGCAGCGAGCGCTCCGCCACCGCGCGCCCGCGCGGAGAGCGG 480
161 ProAlaProLeuGlnPheHisLeuLeuArgAraGlnGlnGlyAspValGlyThr 180
481 CCGGACACACTACAGTTCCACTCTCGCGCGGAATCGCGAGGCGAGCTAGGCGGCAAG 540
181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
541 TCGCGGCTCGTGGACGACGAGCGCGCGCGCTCGGAAAGCGGAGACCGGAGACGAGGAC 600
201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
601 GAAGGAGCTGAGGCGGAGGAGGAGGCGCTCAGTGGTGGCGGAGGAGCGGCGACTGCAA 660
221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
661 GCGGTAGCAGACCCACAGGAACCTGGAAGCATAGAAGAGCGAATTTGTCTCCAGTCAC 720
241 ArgTyrValGluThrMetLeuValAlaAspClnSerMetAlaGluPheHisGlySerGly 260
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781 CTAAAGCATTAACCTTCTCACGTTGTTTTCGCTGGCAGCCGAGATTGTACAAACACCCGCGC 840
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841 ATTCGTAATTCAGTTAGCTGGTGGTGAAGATCTTGTCTATCCACGATGACAGAG 900
301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
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961 CAGCACAAACCCACCCAGTGCAGCGGATGCGAGGCACTATGACACAGCAATCTCTTTTCAACC 1020
341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
1021 AGACAGACTTGTGGGTCCAGACATGATGATCTCTGGGATGGCTGATGTTGGAAC 1080
361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
1081 GTGTGTGATCCGACAGAGCTGCTCGTCCATAGAAGATGATGTTTACAGCTGCTTC 1140
381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
1141 ACCACAGCCCATGAATTAGCCCAAGTGTAAACATGCCACATGATGATGCAAGCAGTGT 1200
401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
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421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
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461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
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481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
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521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
1561 AAATGTGTATCAACCGCAGGTGTGTGAACAAACACGACAGAAAGCATTTTGATAGCCT 1620
541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
1621 TTTTCATGGAAGCTGGGGAATTTGGGGGCTTGGGAGACTGTTTCGAGAACTGCGGTGGA 1680
561 GlyValGluTyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
1681 GGAGTCCAGTACAGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGTAC 1740
581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
1741 TGTGAAGGCAACGAGCTGCGCTACAGATCCTGTAACTTTGAGGACTGTCCAGACAATAAT 1800
601 GlyLysThrPheArgGluGluClnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
1801 GGAAACCTTTTAGAGAGAAACAATGTGAAGCACACACGAGTTTTCAAAGACTTCCCTTT 1860
621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
1861 GGGAGTGGGCTGGGTGGATGGATTCCCAAGTACGCTGGCGTCTCCACAAAGGACAGG 1920
641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
1921 TGCAGCTCATTCGCCAAGCCAAAGCATTTGGCTACTTCTCTGTTTGGAGCCCAAGGT 1980
661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
1981 GTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGTCAGGACAGTGTGTA 2040
681 LysAlaGlyCysAspArgIleLeuAspSerLysLysPheAspLysCysGlyValCys 700
2041 AAAGCTGGTGTGATCGCATCATAGACTCCAAAGAAAGTTTGTATAATGTGTGTGTTGC 2100
701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
2101 GGGGGAATGTGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2160
721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
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741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
2221 CAGAGGGATCCAGGAACAATGGCAGCTTTCTTGCAATCAAGCTGCTGATGGCATAT 2280
761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
2281 ATTTCTAATGGTGACTTACACTTTGTCCACTTAGAGCAAGACATTTATGTACAAAGGTGT 2340
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2341 GTCTTGAGGTACAGCGGCTCTCTCGGCAATGGAAAGAAATTCGAGCTTTTAGCCCTCTC 2400
801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
2401 AAAGAGCCCTTCAGCCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATATAA 2460
821 TyrThrTyrPheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
2461 TACACCTACTTCTGTAAGAGAAAGAAATCTTTCAATGCTATCCCCACTTTTTCAGCA 2520
841 TrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
2521 TGGGTCTATGAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGTGTTGGCAGAGAAGA 2580
861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysLysGluValLys 880
2581 CTGGTAGAATGCCGAGACATTAATGGACAGCGCTGCTCCGAGTGTCCAAAGGAAGTGAAG 2640

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 Db 2821 ATAGACTTTTGCACAATGGCAGATGCAGT 2850

RESULT 3

US-10-115-286-1
 ; Sequence 1, Application US/10115286
 ; Publication No. US20030166065A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jonak, Zdenka
 ; Trulli, Stephen
 ; Fornwald, James
 ; Terrett, Jonathan
 ; Hasting, Gregg

; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Ratner & Prestlia
 ; STREET: Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 04-Apr-2002
 ; APPLICATION NUMBER: US/10/115,286
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/845,496
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestlia, Paul F
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH-70000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169

INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4014 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-115-286-1
 Alignment Scores:
 Pred. No.: 0 Length: 4014
 Score: 5189.00 Matches: 950
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Db: 15 Gaps: 0

US-09-373-658C-2 (1-950) x US-10-115-286-1 (1-4014)
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 Db 577 CTGCTCGCGCGCGCGCTACTGCGCGTGTTCGAGACGACTCGGCGCGCCCTCCGAGGAG 636
 QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
 Db 637 GAGGAGCTAGTGTGTGCGGAGCTGGAGCGCGCGCGGACACGGGACACCGCGCTCCCG 696
 QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluArgProAspSerSerPheLeuAla 80
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 QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
 Db 757 CCGGCTTTCAGCTCCAGAACGTGGCGCGCAATCCGGGTCCGAGACGCGCTTCGGAA 816
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 QY 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThr 180
 Db 957 CCGGCACCACTACAGTTCCACTCTCTCGCGCGAATCGGCAGGGCGACGCTAGGCGGACG 1056
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 QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
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? LOCATION: (450)....(3360)
US-10-105-929-1

Alignment Scores:
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  Pct: 5189.00
  Best Local Similarity: 100.00%
  Query Match: 100.00%
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Db 511 ATGGGAACCGCGAGCGGCTCCGGGCTCTGGAGCTTTGGGCGCGTACCCAGCTGCTG 570

QY 21 LeuLeuAlaAlaAlaLeuLeuValSerAspAlaLeuGluArgProSerGluGluAsp 40
Db 571 CTGCTCCGCGCGGCTACTGGCCGTGTCCGACGCTCTGGGCGCGCTCCGAGGAGGAC 630

QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
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QY 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
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APPLICANT: Peterson, Carsten
 APPLICANT: Meltzer, Paul
 TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
 TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
 FILE REFERENCE: 11613.56US11
 CURRENT APPLICATION NUMBER: US/10/159,563
 CURRENT FILING DATE: 2002-12-09
 PRIOR APPLICATION NUMBER: US 10/133,937
 PRIOR FILING DATE: 2002-04-25
 NUMBER OF SEQ ID NOS: 444
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 192
 LENGTH: 4459
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-159-563-192

Alignment Scores:
 Pred. No.: 0 Length: 4459
 Score: 5181.00 Matches: 949
 Percent Similarity: 99.89% Conservative: 0
 Best Local Similarity: 99.89% Mismatches: 1
 Query Match: 99.85% Indels: 0
 DB: 16 Gaps: 0

US-09-373-658C-2 (1-950) x US-10-159-563-192 (1-4459)

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 QY 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrArgLeuArg 60
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RESULT 7
US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 308
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-308
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Score: 5181.00 Matches: 949
Percent Similarity: 99.89% Conservative: 0
Best Local Similarity: 99.89% Mismatches: 1
Query Match: 19.85% Indels: 0
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US-09-373-658C-2 (1-950) x US-10-159-563-308 (1-4459)

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QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
DB 2154 GGGAGTGGCCCTGCGGTGGAAATGCAATCCCAAGTACGCTGCGCTCTCACCAAGACACAGG 2213
QY 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
DB 2214 TGCAGCTCATCTGCCAAGCCAAAGGATTTGGCTACTTCTTGTTTTGCAGCCCAAGTT 2273
QY 561 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
DB 2274 GTAGATGGTACTCCATGTAGCCCAAGATTCACCTCTGTGTGTGCAAGACAGTGTGTA 2333
QY 681 LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys 700
DB 2334 AAAGCTGGTGTGATCGCATCATAGACTCCAAAAGAGTTTGATAAATGTGGTGTTC 2393
QY 701 GlyLysAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
DB 2394 GGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTACTAGTCANAACTTGA 2453
QY 721 TyrHisAspIleIleThrIleProThrGlyValAlaThrAsnIleGluValLysGlnArgAsn 740
DB 2454 TATCATGATATCATCAATTCACATCGGAGCCACCAACATCGAAGTGAACACGCGAAC 2513
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
DB 2514 CAGAGGGATCCAGGAACAATGCGCAGCTTCTTTCGCTCAAACTCTGATGCCACATAT 2573
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
DB 2574 ATTCCTTAATGGTGACTACACTTTGTCCACCTTAGACACAAGACATATGTACAAAGTGT 2633
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
DB 2634 GTCTTGAGGTACAGCGCTCTCTGCGGCATTTGGAAGAAATTCGACAGCTTTAGCCCTCTC 2693
QY 801 LysGluProIleuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
DB 2694 AAAGAGCCCTTGACCATCCAGGTCTTCTACTGTGGCAATGCCCTTCGACCTAAATTA 2753
QY 821 TyrThrTyrPheValLysLysLysGlySerPheAsnAlaIleProThrPheSerAla 840
DB 2754 TACACTACTTGTGAAGAGAGAGAGGAAATCTTTCAATGCTATCCCACTTTTCAGCA 2813
QY 841 TrpValIleGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
DB 2814 TGGGTCAATGAAGAGTGGGGCAATGTTCTAAGTCATGTGAATTCGGTTGGCAGAGAAGA 2873
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 880
DB 2874 CTGGTAGAATGCCGAGACATTAATGGACAGCTCTGCTCCGAGTGTGCAAGAGTGAAG 2933
QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
DB 2934 CCAGCAGCAGCAGACCTTGTGACAGACCATCCCTGCCCCCAGTGGCAGCTGGGGAGTGG 2993
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
DB 2994 TCATCATGTTCTAAGACCTGTGGGAAGGGTTACAAAAAAGAGCTTGAAGTGTCTGTCC 3053
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940

Db 3054 CATGATGGAGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTAAACATTT 3113
Qy 941 IleAspPheCysThrMetAlaGluCysSer 950
Db 3114 ATAGACTTTTGCACAATGGCAGATGCAGT 3143
RESULT 8
US-09-971-429B-17
; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shvian, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971.429B
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-971-429B-17
Alignment Scores:
Pred. No.: 0 Length: 4760
Score: 5181.00 Matches: 949
Percent Similarity: 99.89% Conservative: 0
Best Local Similarity: 99.89% Mismatches: 1
Query Match: 99.85% Indels: 0
DB: 10 Gaps: 0
US-09-373-658C-2 (1-950) x US-09-971-429B-17 (1-4760)
Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 612 ATGGGGAAACGGAGACGGGCTCCGGGCTCGGAGCTTTGGGCCAGTACCCACGCTGCTG 671
Qy 21 leuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db 672 CTGCTCGCGCGGCTACTGGCGCTGTGGAGACGACTCGGGCGCCCTCCGAGGAGGAC 731
Qy 41 GluGluLeuValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db 732 GAGGAGCTAGTGTGCGGAGCTGGAGCGGCCCGGGACACGGGACACACGCGCTCCGC 791
Qy 61 leuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProSerSerPheLeuAla 80
Db 792 CTGCACGCTTTTGACGACGCTGATCTGGAGCTGCGCGCGGACGACGCTTTTGGCG 851
Qy 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 852 CCCGGCTTCAGCTCCAGACAGTGGGGCGCAAAATCCGGGTCCGAGACGCGCTTCGGAA 911
Qy 101 ThrAspLeuAlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 912 ACCGACCTGGGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 971
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyThrLeuGlyGluAlaTyPhe 140
Db 972 GCCCTACGCTCTGCGAGGGCGTTCGGCGCGCTTCTACTGCTGGGGGAGCGGTATTTC 1031

Qy 141 IleGluProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 1032 ATCCAGCCGCTGCCCGCCAGCAGCGCTCGCCACCGCCCGCCAGGGAGAACCG 1091
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr 180
Db 1092 CCGGCACCACTACAGTTCACCTCTCTCGGCGGAATCGGCGGCGAGCTAGCGGCGACG 1151
Qy 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 1152 TGGGGGTCTGTGACGACGAGCCCGCGGCTCGGAGAAAGCGGAGACCGAAGACGAGGAC 1211
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 1212 GAAGGAGCTGAGGGCGAGGACGAGGGGCTCAGTGTCTCGCGGAGGACCGCGGACTGCAA 1271
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHis 240
Db 1272 GCGGTAGGACAGCCACAGGAAGCTGGAAGCATAGAAAGAGCGATTTGTGTCCAGTCCAC 1331
Qy 241 ArgTyrrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1332 CGCTATGTGGAAACCATGCTTGTGGCAGACCACTCGATGGCAGAAITTCACGGCAGTGGT 1391
Qy 261 LeuLysHisTyrrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrrLysHisProSer 280
Db 1392 CTAAGCATTACCTTCTCAGTTGTTCGTGGCAGCCAGATTTGTACAAACACCCCGACG 1451
Qy 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1452 ATTCTGTAATTCAGTTAGCTGTGGTGTGAAGATCTTGTTCATCCACGATGAACAGAAG 1511
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1512 GGGCGGGAAGTGAACCTCCATGCTGCTCCCTCACCTCGCGAAGCTTTTGCRACTGGCAGAAG 1571
Qy 321 GlnHisAsnProSerSerArgAspAlaGluHisTyrrAspThrAlaIleLeuPheThr 340
Db 1572 CAGCACAAACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATTTCTTTTACC 1631
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1632 AGACAGGACTTGTGTGGTCCACAGCATGTGATCTTTGGGATGCTGATGTGGAACT 1691
Qy 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPhe 380
Db 1692 GTGTGTGATCCGAGCAGAAAGCTGCTCCGTATAGAAAGATGATGTTTACAAAGCTGCTTC 1751
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCys 400
Db 1752 ACCACAGCCCATGAATTAGCCACCGTGTATACATGCCACATGATGATGCAAGAGCTGT 1811
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1812 GCCAGCCTTAATGCTGTGAACGAGGATTCACCATGATGCGCTCAATGCTTTTCCAACCTG 1871
Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrrMetIleThrSerPheLeuAspAsn 440
Db 1872 GACCACAGCCAGCTGTGCTCTCTTCAGTGGCTACATGATACATCATTTCTGGATAAT 1931
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1932 GGTGATGGGAATGTTGATGGACAGCTCAGAAATCCCATACAGCTCCACAGGGATCTC 1991
Qy 461 ProGlyThrSerTyrrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db 1992 CTTGGCACCTCGTACCATGCCAACCGGAGTGCAGTTTACATTTGCGGAGGAGCTCCAAA 2051
Qy 481 HisCysProAsnAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db 2052 CACTGCCCCGATGCACCCAGCAGCATGATGACACCTTGTGTGTATCCGCGACCTCTGTTGG 2111

QY 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
DB 2112 GTCCTGGTGTGCAAAACCAACACTCCCGTGGCGGATGGCCACGCTGTGGAGAGG 2171
QY 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
DB 2172 AAATGGTGATCAACCGCAAGTGTGTGAACAAACCCGACAGAAAGCATTTTCATACGCT 2231
QY 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
DB 2232 TTTCATGAAGCTGGGAATGTGGGGCTTGGGGAGACTGTTCAGAACCTGGCGTGA 2291
QY 561 GlyValGlnTrpMetArgGluCysAspAsnProValProLysAsnGlyLysTyr 580
DB 2292 GGAGTCCAGTACACGATCAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAATAC 2351
QY 581 CysGluGlyLysArgValArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
DB 2352 TGTGAAGCAACAGAGTGGCTACAGATCCCTGTAACTTGAGGACTGTCCAGACAATAAT 2411
QY 601 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
DB 2412 GGAATAACCTTAGAGAGCAATGTGANGACACACACGAGTTTCAAAGCTTCCTTT 2471
QY 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
DB 2472 GCGAGTGGGCTGGCGTGGAAATGGAATCCCAAGTACGCTGGCTCTCAACCAAGACAGG 2531
QY 641 CysLysLeuIleCysGluAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
DB 2532 TGCAGCTCATCTGCCAGCCAAAGGCATTGGCTACTTCTCGTTTTCAGCCCAAGGTT 2591
QY 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyCysVal 680
DB 2592 GTAGATGGTACTCCATGTAGCCCAATCCACCTCTGTCTGTGCAAGGACAGTGTGTA 2651
QY 681 LysAlaGlyCysAspArgIleLeuAspSerLysLysPheAspLysCysGlyValCys 700
DB 2652 AAAGCTGTGTGATCGCATATAGACTCCAAAGAAAGCTTTGATAAATGGTGTTC 2711
QY 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
DB 2712 GGGGAAATGGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGCAAAACCTGGA 2771
QY 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGluArgAsn 740
DB 2772 TATCATGATATCATCACAAATCCAACTGGAGCCCAACATCGAAGTGAACACGCGAAC 2831
QY 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
DB 2832 CAGAGGGATCCAGGAACAATGGCAGCTTTCTGCCATCAAGCTGCTGATGGCACATAT 2891
QY 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
DB 2892 ATTTCTTAATGGTGACTACACTTTGTCCACTTAGAGCAAGACATTTATGACAAAGGTGT 2951
QY 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
DB 2952 GTCTTGAGTACAGCGGCTCTCTCGCGCATGTGAAAGAAATCCGAGCTTTAGCCCTC 3011
QY 801 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 820
DB 3012 AAAGAGCCCTTGACCATCCAGTCTTACTGTGGGCAATGCCCTTCGACCTTAAATAATAA 3071
QY 821 TyrThrTyrPheValLysLysGlySerPheAsnAlaIleProThrPheSerAla 840
DB 3072 TACACCTACTTCTGTAAGAAGAAAGAAATCTTTCAATGATATCCCCACCTTTTTCAGCA 3131
QY 841 TrpValIleGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 860
DB 3132 TGGGTCAATTGAAGAGTGGGCGAATGTTCTTAAGTCATGTGAATGGGTGGCAGAGAAGA 3191
QY 861 LeuValGluCysArgAspIleAsnGlyGlnProLysSerGluCysAlaLysGluValLys 880

DB 3192 CTGGTAGAATGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTGCAAGGAAGTGAAG 3251
QY 881 ProLysSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
DB 3252 CCAGCCAGCACAGACCTTGTGCAGACCATCTCCCTGCCCCAGTGGCAGCTGGGGAGTGG 3311
QY 901 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysArgSerLeuLysCysLeuSer 920
DB 3312 TCATCATGTTCTTAAGACCTGTGGAGGGTTACAAAAAAGAGCTTGAAGTGTCTCTCC 3371
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
DB 3372 CATGATGGAGGGTGTATTATCTCATGAGCTGTGATCTTTAAAGAAACCTTAACATTC 3431
QY 941 IleAspPheCysThrMetAlaGluCysSer 950
DB 3432 ATAGACTTTTGCACATGGCAGAAATGCAGT 3461
RESULT 9
US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)
; OTHER INFORMATION:
US-09-989-687-125
Alignment Scores:
Pred. No.: 0 Length: 4014
Score: 5144.00 Matches: 940
Percent Similarity: 99.37% Conservative: 4
Best Local Similarity: 98.95% Mismatches: 6
Query Match: 99.13% Indels: 0
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DB 517 ATGGGGAACCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGGCCGTACCCACGCTGCTG 576
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
DB 577 CTGCTCGCCGCGCGCTACTGGCGGTGCGAGCGACTCGGGCGCCCTCCGAGGAGGAC 636
QY 41 GluGluLeuValValProGluLeuArgAlaProGlyHisGlyThrThrArgLeuArg 60
DB 637 GAGGAGCTAGTGTGCGGAGCTGGAGCGCTCCCGGACACCGGACACGCGCCCTCCG 696
QY 61 LeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80
DB 697 CTGCAGCCTTTGACGACGACGCTGGATCTGGAGCTGCGCGCCGACGACGAGCTTTTGGCG 756
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlyThrProLeuProGlu 100
DB 757 CCGCGCTTACGCTCCAGAACGTTGGGGCGCAATCCGGGTCCGACACCCCGCTTCCGGA 816
QY 101 ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla 120

Db 817 |||||ACCGACTCGCGCACTGCTTCTACTCCGCGACCGTGAATGGCGATCCCAAGCTCGGCTGC 876
Qy 121 AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe 140
Db 877 GGCCTCAGGCTCTGCGAGGCGCGTGCAGCGCGCTTCTACTGCTGGGGAGCGTATTTC 936
Qy 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro 160
Db 937 ATCCAGCGCTGCCCGCGCGAGGAGCGCTCGCCACCGCGCGCCAGGGAGAGCGG 996
Qy 161 ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlnGlyAspValGlyThr 180
Db 997 CGCGCACCACTACAGATTCCACTCTCTGCGCGGGAATCGCGAGCGGAGCTAGCGCGCACG 1056
Qy 181 CysGlyValValAspAspGluProAspProThrGlyLysAlaGlnThrGluAspGluAsp 200
Db 1057 TGGCGGGTCTGTGACGACGAGCCCGCGCGACTGGGAGGAGCGAGACCGAAGCGAGAC 1116
Qy 201 GluGlyThrGluGlyGluAspGluGlyProGlnInTrpSerProGlnAspProAlaLeuGln 220
Db 1117 GAAGGACTGAGGGCGAGGACGAAGGGCTCTAGTGGTCCGCGAGGACCGCGCACTGCAA 1176
Qy 221 GlyValGlyGlnProThrGlyThrGlySerIleAtdLysValArgPheValSerSerHis 240
Db 1177 GCGTAGGACAGCCACGGAATGGAAGCATAGAAGAGAGCGATTTGTGTCAGTCTAC 1236
Qy 241 ArgTyrValGlnThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1237 CGCTATGTGMAACCATGCTTGTGGCAGACCAGTCTGATGGCAGATTTCCACGGCAGTGT 1296
Qy 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db 1297 CTAAAGCATTAACCTTCTCACTGTTGTTTCGGTGGCAGCGAGATTGTACAAACCCCCAGC 1356
Qy 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1357 ATTCGTAAATCAGTAGCTGCTGGTGGTGAAGATCTTGGTCACTCCACCATGACAGAG 1416
Qy 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1417 GCGCCCGAAAGTCACTCCCAATGCTGCGCTCACTCTCGGAACTTTTGAACCTGGCAGAG 1476
Qy 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db 1477 CAGCACACCCAGCCAGTACCGGATGACAGACACTATGACACAGCAATCTTTTCACC 1536
Qy 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1537 AGACAGACTTGTGTGGTCCCGACATGTGATCTCTTGGATGGCTGATGTGAACT 1596
Qy 361 ValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaPhe 380
Db 1597 GTGTGTATCCGAGCAGAGAGCTGCTCCGTCATAGAAGATGATGGTTTCAAGTGGCTTC 1656
Qy 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db 1657 ACCACAGCCCATGAATTAGCCACAGTGTTAACATGCCACATGATGCMAAGCAGTGT 1716
Qy 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1717 GCCAGGCTTAATGGTGTGAACCCAGGATCCCATGATGGCGTCAATGCTTTTCAACCTG 1776
Qy 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440
Db 1777 GACCACAGCCAGCTTGGTCTCTCTGAGTGGCTACATGAATACATCATTTCTGGATAT 1836
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1837 GGTCAATGGGGAATGTTTGTAGGCAAGCCCTCAGAAATCCCATACAGCTCCCGCGCATCTC 1896
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480

Db 1897 CCTGCACCTCGTACGATGCCCAACGGCGAGTGCACAGTTTACATTTGGGAGGACTCCAAA 1956
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 500
Db 1957 CACTGCCCTGHTGACAGCCAGCACATGTAGCACTTGTGTGTACCGGCACCTCTGGTGG 2016
Qy 501 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 520
Db 2017 GTGCTGGTGTGTCAAAACCAACCACTTCCGCTGGCGGATGGCACCAGCTGTGGAGAGG 2076
Qy 521 LysTrpCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAspThrPro 540
Db 2077 AAATGGTGTATCAACCGCAAGTGTGTGAACAAACACACAGAAAGCATTTTGTATCGCT 2136
Qy 541 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 560
Db 2137 TTTTCATGGAAGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACGTCGGGTGA 2196
Qy 561 GlyValGlnThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyr 580
Db 2197 GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGAGATAC 2256
Qy 581 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsn 600
Db 2257 TGTGAAGCAACAGTGGCTTACAGATCTTGTAACTTGAGGACTGTCCAGACATAAT 2316
Qy 601 GlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 620
Db 2317 GGAATAAACCTTTAGAGAGGAAATGTGAAGCACACAAACGAGTTTTCAAAAGCTTCCTTT 2376
Qy 621 GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg 640
Db 2377 GGGAGTGGGCTCGGTGGATGGATTTCCAAAGTACGCTGGCGTCTCACCAGGACAGG 2436
Qy 641 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 660
Db 2437 TGCAGCTCATCTGCAAGCCAAAGGCATTTGGCTACTTCTTCGTTTTCAGGCCAAGGT 2496
Qy 661 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysVal 680
Db 2497 FTAGATGTACTTCCATGTAGCCCGATTTCCACTCTGCTGTGTGCAAGGACAGTGTGA 2556
Qy 681 LysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCys 700
Db 2557 AAAGCTGTTGTGATCGCATCATAGCTCCAAAGAAAGTTTGTATAATGTGGTGTTCG 2616
Qy 701 GlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGly 720
Db 2617 GGGGGAAATGGATCTACTTGTAAAAAATAACAGATCAGTTACTAGTGTGCAAAACCTGA 2676
Qy 721 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 740
Db 2677 TATCATGATATCATCAATTCCAACTGGAGSCCAACATCGAAGTGAACAGCGGAAC 2736
Qy 741 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 760
Db 2737 CAGAGGGATCCAGGAACAATGGCAGCTTTCTTGCCATCAAGAGCTGTGTGTGGCACAT 2796
Qy 761 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 780
Db 2797 ATTCTTAATGTGACTACACTTTGTCCACCTTAGGCAAGACATTTATGTACAAGGTGTT 2856
Qy 781 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 800
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Db 2917 AAAGAGCCCTTGACCATCAGGTTCTTACTGTGGCAATGCCCTTCGACTTAATAATTA 2976
Qy 821 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 840
Db 2977 TACACTTACTTCGTAAGAAGAGAGAAATCTTTCAATGCTATGCCACATTTTTCAGCA 3036

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QY 861 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaIysGluVallys 880
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QY 881 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 900
Db 3157 CCAGCCAGACACAGACCTTGTGCAGACCATCCTGCCCCCGAGTGGCAGCTGGGGAGTGG 3216
QY 901 SerSerCysSerLysThrCysGlyLysGlyTrpLysLysArgSerLeuLysCysLeuSer 920
Db 3217 TCATCATGTGTTAAGACCTGTGGGAAGGGTTACAAAAAACAAGCTTGAAGTGTCTGTCC 3276
QY 921 HisAspGlyGlyValLeuSerHisGluSerCysAspProLeuLysLysProLysHisPhe 940
Db 3277 CATGATGAGGGGTGTATCTCATGACAGCTGTGATCTTTAAAGAAACCTTAACATTTTC 3336
QY 941 IleAspPheCysThrMetAlaGluCysSer 950
Db 3337 ATAGACTTTTGCAATGCGAGATGCAGT 3366

RESULT 10
US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851

Alignment Scores:
Pred. No.: 0 Length: 4848
Score: 5097.50 Matches: 949
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 98.24% Indels: 73
Db: 13 Gaps: 1

US-09-373-658C-2 (1-950) x US-10-425-114-26851 (1-4848)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 493 ATGGGGAACGGAGCGGGCTCCGGGGTCTCGAGCTTTGGCCCGTACCCACGCTGCTG 552
QY 21 LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 40
Db 553 CTGCTCGCGCGGGCTACTGGCGGTGTCGAGCGACCTCGGGCGCCCTCGGAGAGGAC 612
QY 41 GluGluLeuValValProGluLeuGluArgAlaProGlyHisGlyThrThrArgLeuArg 60
Db 613 GAGGAGCTAGTGGTCCCGAGCTGGAGCGCGCCCGGACACCGGACCGCGCTCCGC 672
QY 61 LeuHisAlaPheAspGlnLeuAspLeuGluLeuArgProAspSerSerPheLeuAla 80

Db 673 CTGCACGCTTTGACACGACAGCTGCATCTCGAGCTGGCGCCGACAGCAGCTTTTGGCG 732
QY 81 ProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThrProLeuProGlu 100
Db 733 CCCGCTTCACGCTCCAGACAGTGGGGCGAAATCCCGGTCGAGAGCCGCTTCGCGAA 792
QY 101 ThrAspLeuAlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAla 120
Db 793 ACCGACCTGGCGCACTGCTTCTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTGCC 852
QY 121 AlaLeuSerLeuCysGluGlyValArgGlyValPheTyLeuLeuGlyGluAlaTyPhe 140
Db 853 GCCCTCAGCCTTCTCGAGGGCGTGGCGGCGCTTCTACCTGCTGGGGAGCGGTATTC 912
QY 141 IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlyLysPro 160
Db 913 ATCCAGCGCTGCCCGCGCGACGAGCGCTGCGCACCGCGCCCGAGGGAGAGCGG 972
QY 161 ProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyThr 180
Db 973 CCGGCACCATCTACAGTTCCACCTCCTCGCGCGAATCGGAGGCGGACGCTAGGCGGACG 1032
QY 181 CysGlyValValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAsp 200
Db 1033 TCGGGGTGGTGACGACGAGCGCCCGCGCTGGGAAAGCGGAGACCGAAGACGAGGAC 1092
QY 201 GluGlyThrGlnGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln 220
Db 1093 GAGGGACTCGAGGGCGAGGAGCGAAGGGCTCAGTGGTGGCGGAGGACCGGCACTGCA 1152
QY 221 GlyValGlyGlnProThrGlyThrGlySerIleArgLysArgPheValSerSerHis 240
Db 1153 GCGTAGGACAGCCACAGGAACCTGGGAAGCATAGAAGAAGCGATTTGTCTCAGTCA 1212
QY 241 ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly 260
Db 1213 CGCTATGTGAAACCATGCTTGTGGCAGACGAGTCGATGCGAGAAATTCACGCGAGTGT 1272
QY 261 LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer 280
Db 1273 CTAAGCATTTACCTTCTCAGCTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCGAG 1332
QY 281 IleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 300
Db 1333 ATTCGTAATTCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAACAGAG 1392
QY 301 GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 320
Db 1393 GGGCGGAAGTGACCTCCAAATGCTGCCCTCACTCTCGGAACTTTGCAACTGGCAGAAG 1452
QY 321 GlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr 340
Db 1453 CAGCACAACCCACCCAGTGAGCCGGGATGCAGAGCACTATGCACACAGCAATTCITTTACC 1512
QY 341 ArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr 360
Db 1513 AGACGAGACTTGTGTGGGTCCGACATGTGATCTCTGGGATGGCTGTGTGGAACT 1572
QY 361 ValCysAspProSerArgSerCysSerValIleLeuAspAspGlyLeuGlnAlaAlaPhe 380
Db 1573 GTGTGTGATCCGAGCAGAGCTGCTCGTCTATAGAGATGATGGTTTACAGTGCCTTC 1632
QY 381 ThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys 400
Db 1633 ACCACAGCCCATGAATTAGGCCACGTTTAAACATGCACATGATGATGCAAGACAGTGT 1692
QY 401 AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu 420
Db 1693 GCACGCTTAAATGGTGTGAACACGAGATTCACATGATGGCGTCAATGCTTTCCAACTG 1752
QY 421 AspHisSerGlnProTrpSerProCysSerAlaTyrMetIleThrSerPheLeuAspAsn 440

Db 1753 GACCACAGCCAGCCTTGGTCTCCTGTCAGTGCCTACATGATTACATCAATTTCTGGATAAT 1812
Qy 441 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 460
Db 1813 GGTCAATGGGAATGTTTGGATGGCAAGCCTCAGAATCCATA-CAGCTCCCGAGCGATCTC 1871
Qy 461 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 480
Db 1872 CTTGGACCTCGTACGATGCGACACCGGAGTGCAGTTTCAATTTGGGGAGGACTCCAAA 1931
Qy 481 HisCysProAspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThrSerGlyGly 500
Db 1932 CACTGCCCTCATGCGAGCAGCACATGTAGCACCTTGTGGTACCGGCACCTCTGGTGGG 1991
Qy 501 ValLeuValCysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGly 520
Db 1992 GTGCTGTGTGTCAAAACCAACACTTCCCGTGGCGGATGCGACCACTGTGGAGAGGG 2051
Qy 521 LysTyrCysIleAsnGlyLysCysValAsnLysThrAspArgLysHisPheAsp----- 538
Db 2052 AAATGGTGTATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTTGATGTGAGT 2111
Qy 538 ----- 538
Db 2112 TTTTCTACTGAACACATTCAGAAATTGAAAGAAACAAAGTGTGTTAAAGATATGATAC 2171
Qy 538 ----- 538
Db 2172 CAAGTTAAACATCCCAATCCGTCTCTAGCAGGAATGCGAGATGCTTAATTTTAGAA 2231
Qy 538 ----- 538
Db 2232 CTGATTTCTTGTCCATGTCCTTCTTGATACCTTAAAGTTCTCTTTAGATAAATCT 2291
Qy 539 -----ThrProPheHisGlySerTyrGlyMetTyrGly 549
Db 2292 AATGCTGATGATTTATGCTCTCCATTTAGACGCTTTTTCATGGAAAGCTGGGGAATGGGG 2351
Qy 549 yProTyrGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCys 569
Db 2352 GCCTTGGGAGACTTTCGAAAGCTGCGGTGGAGGAGTCCAGTACACGATGAGGGAATG 2411
Qy 569 sAspAsnProValProLysAsnGlyLysTyrCysGluGlyLysArgValArgTyrArg 589
Db 2412 TGACAAACCCAGTCCCAAGAAATGAGGGAAGTACTGTGAAGGCAAAACGATGCGCTACAG 2471
Qy 589 gSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCys 609
Db 2472 ATCTGTAACTTTGAGGACTGTCCAGCAATATGGAAACCTTTAGAGAGAAACATG 2531
Qy 609 sGluAlaHisAsnGlnPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIle 629
Db 2532 TGAAGCACACACAGAGTTTTTCAAAAGCTTCTTTGGAGTGGGCTGCGGTGGAATGGAT 2591
Qy 629 eProLysTyrAlaGlyValSerProLysAspArgCysValLysLeuIleCysGlnAlaLysGly 649
Db 2592 TCCCAAGTACCTGGCTGTCCACAAAGGACAGTGCAGCTCATCTGCCAACCCAAAGG 2651
Qy 649 yIleGlyTyrPhePheValLeuGlnProLysValAlaAspGlyThrProCysSerProAs 669
Db 2652 CATTTGGTACTTCTCTGTTTGGAGCCCAAGTTGTAGATGGTACTCCATGTAGCCACGA 2711
Qy 669 pSerThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleLeuAs 689
Db 2712 TTCACCTCTCTGTGTGCAAGACAGTGTGTAAGCGTGGTGTGATCGCATCATAGA 2771
Qy 689 pSerLysLysPheAspLysCysGlyValCysGlyValCysGlyAsnGlySerThrCysLysLys 709
Db 2772 CTCCAAAAAGAGTTGATAAATGTGGTGTTCGGGGGGAATGGATCTACTTGTAAAAA 2831
Qy 709 sIleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProth 729
Db 2832 AATATCAGGATCAGTTACTAGTGCAAACCTGGATATCATGATATCATCAATTCACAC 2891

Qy 729 rGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySe 749
Db 2892 TGAGAGCACCAACATCGAAGTGAACACAGCGGAACACAGAGGGGATCCAGGAACAAATGGCAG 2951
Qy 749 rPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSe 769
Db 2952 CTTTCTTGGCATCAAGCTGCTGATGGCACATATATCTTAAATGGTGACTACTTGTTC 3011
Qy 769 rThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAl 789
Db 3012 CACTTTAGACGAAGACATTTATGTACAAAGTGTGTCTTGAGGTACAGCGCTCTCTGTC 3071
Qy 789 aAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLe 809
Db 3072 GCGTTTGGAAAGATTCGACAGCTTTAGCCCTCTCAAAAGAGCCCTTCACCATCCAGGTTCT 3131
Qy 809 uThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLys 829
Db 3132 TACTGTGGGCAATGCCCTTCGACCTTAAATTAATAACACTACTTCTGTTAAAGAGAAGAA 3191
Qy 829 sGluSerPheAsnAlaIleProThrPheSerAlaTyrValIleGluGluTyrGlyGluCys 849
Db 3192 GGAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAATGAAGAGTGGGGCGAATG 3251
Qy 849 sSerLysSerCysGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGly 869
Db 3252 TTCTAAGTCATGTAATTCGGTGGCAGAGAAGACTGGTAGAATGCCGAGACATTAATGG 3311
Qy 869 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 889
Db 3312 ACAGCCTGCTTCGAGTGTGCAAAAGAGTGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3371
Qy 889 pHisProCysProGlnTyrGlnLeuGlyGluTyrPheSerCysSerLysThrCysGlyLys 909
Db 3372 CCATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTCACTATGTTCTAAGACCTGTGGAA 3431
Qy 909 sGlyTyrLysLysArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGly 929
Db 3432 GGGTTACAAAAAAGAAAGCTTGAAGTGTCTGCCATGATGAGGGGTGTATCTCATGA 3491
Qy 929 uSerCysAspProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCys 949
Db 3492 GAGCTGTGATCTCTTTAAAGAAACCTTAAACATTTTCATAGACTTTTTCACCAATGGCAGAATG 3551
Qy 949 sSer 950
Db 3552 CAGT 3555
RESULT 11
US-09-373-658-20
; Sequence 20, Application US/09373658
; Publication NO. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Ituela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka I.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fromwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1489.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4180
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown

US-09-373-658-20

Alignment Scores:

Pred. No.: 0
Score: 4289.50
Percent Similarity: 88.31%
Best Local Similarity: 82.36%
Query Match: 82.86%
DB: 10
Length: 4180
Matches: 789
Conservative: 57
Mismatches: 97
Indels: 15
Gaps: 5

US-09-373-658C-2 (1-950) x US-09-373-658-20 (1-4180)

QY	1	MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu	20
DB	441	ATGGGGAGCTCCAGCGGGCAGCGAGATCTCGGGGCTCTCTGTCGCCACACATGCTGTG	500
QY	21	LeuLeuAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer	37
DB	501	CTGCTCTCTGCTTCCATAACAAGCTGCTATGTGCGCGGGCGCACACACGGGGCCCG	560
QY	38	GluGluAspGluGluLeuValProGluLeuGluArgAlaProGlyHisGly-----	55
DB	561	GAGGAGATGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	620
QY	56	ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp	75
DB	621	ACCACAGCGCTTCTGTCAGCGCTTTGGCCAGCAGCTACATCTGAAGTTGACGCGGAC	680
QY	76	SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerGlu	95
DB	681	AGCGGTTCCTGCGCGCTGCTCTACCTCTGACAGCTGTGGGGCGCAGTCCCGGTCCGAG	740
QY	96	ThrProLeu-----ProGluThrAspLeuAlaHisCysPheTy-SerGlyThrValAsn	113
DB	741	GCACAACATCTGGACCCACCGGGGACCTGGCTCCTCTCTCTGCGACGGTAAAC	800
QY	114	GlyAspProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTy	133
DB	801	GGTGATCCCGGCTGTCGCCAGCCCTCAGCTCTGTGAAGGTGTGCTGCTGCTCTAC	860
QY	134	LeuLeuGlyGluAlaTyPheLeuGlnProLeuPro---AlaAlaSerGluArgLeuAla	152
DB	861	CTACAGGAGAGAGGTTCCTTCATTGACGCGCTGGAGTGCGCCACCGCGCTGGCC	920
QY	153	ThrAlaAlaProGlyGluTyProAlaProLeuGlnPheHisLeuLeuArgAsn	172
DB	921	CCTGCGCTGCCGAGGAGGATCATCCGACCGCGCGCTGCTCCATCTCTGAGGCGAAG	980
QY	173	ArgGlnGlyAspValGlyTyThrCysGlyValValAspAspGluProArgProThrGly	192
DB	981	CGCGGGGAGTGGCGGCGCCAAAGTGGCGGCTATGGACGACGAGACCCCTGCCAAC	1037
QY	193	LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrp	212
DB	1038	-----AGCGACTCGCGACCGGAGCGCAGAACACCCCGGAACCACTGG	1079
QY	213	SerProGlnAspProAlaLeuGlnGlyValGlnProThrGlyThrGlySerIleArg	232
DB	1080	CCTGTGCGGAGACCCACCGCTCAGGACCGCGGAAAGCCATCAGGACCGAGGAGTAAG	1139
QY	233	LysLysArgPheValSerHisArgTyValGluThrMetLeuValAlaAspGlnSer	252
DB	1140	AAGAAGCATTTGTCTCAGCCCGCTTATGTGGAACCACTGCTGAGTGTGACAGTCC	1199
QY	253	MetAlaGluPheHisGlySerGlyLeuLysHisTyThrLeuLeuThrLeuPheSerVala	272
DB	1200	ATGGCGGACTTCCAGCGGCGGTCTAAAGCATTAACCTTCTAAACCTGCTCTCGGTGCA	1259
QY	273	AlaArgLeuTyLysHisProSerIleArgAsnSerValSerLeuValValIleValle	292
DB	1260	GCCAGGTTTACAGCATCCAGCATTAAGGATTAATGATGCTGGTGGTGGTGAATC	1319
QY	293	LeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeu	312

DB	1320	TTGGTCATATACGAGGAGCAGAGGAGCCAGAGGTACCTCCATGACGCTCTCACCTT	1379
QY	313	ArgAsnPheCysAsnTrpClnLysGlnHisAsnProProSerAspArgAspAlaGluHis	332
DB	1380	CGGAATTTCTGAGCTGGCAGAAACACACACACCCCGAGTGCAGGATCCAGAGCAC	1439
QY	333	TyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThr	352
DB	1440	TATGACACTGCAATCTGTTTACACAGACAGGATTTATGTGGCTCCACACGTTGACACT	1499
QY	353	LeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGlu	372
DB	1500	CTCGGAATGGCAGATGTTGGAAACCGTATGTGACCCAGCAGAGCTGCTCAGTCATAGAA	1559
QY	373	AspAspGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisValPheAsnMet	392
DB	1560	GATGATGTTTGCNAGCGCTTACACACAGCCCATGATTTGGGCAATGTGTTTACATG	1619
QY	393	ProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMet	412
DB	1620	CGGCACGATGATGCTTAAGCAGCTGTGCCAGCTTGAATGTTGAGTGGGATTTCTCATCTG	1679
QY	413	MetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTy	432
DB	1680	ATGGCTCTGATGCTCTCCAGCTTAGACCATAGCCAGCCCTGCTCAGCTTGCAGTGCCTAC	1739
QY	433	MetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsn	452
DB	1740	ATGGTCAGCTCTCTTAGATAATGACACCGGAAATGTTTGTGATGACACAGCCCGAAT	1799
QY	453	ProIleGlnLeuProGlyAspLeuProGlyThrSerTyAspAlaAsnArgGlnCysGln	472
DB	1800	CCATCAAGCTCCCTTCTGATCTTCCCGGTACCTTGTACGATGCCAACCGGAGTGTGAG	1859
QY	473	PheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeu	492
DB	1860	TTTACATTCGAGAGGATCCCAAGCAGCTCCCTGATGACGACGACATGATACCTG	1919
QY	493	TrpCysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAla	512
DB	1920	TGGTGACCTGCGACCTCCGTTGCTTACTGTTGTCGCAAGTGTGCTGCTGCTGCTGCA	1979
QY	513	AspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysThr	532
DB	1980	GATGACACAGCTGTGGAGAGGAGGAGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCA	2039
QY	533	AspArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGly	552
DB	2040	GACATGAAGCATTTTGTCTCTCTGTTTATGGAAGCTGGGAGCCATCGGAGCCGCTGGA	2099
QY	553	AspCysSerArgThrCysGlyGlyValClnTrpThrMetArgGluCysAspAsnPro	572
DB	2100	GACTGCTCAAGAACCTGT	2159
QY	573	ValProLysAsnGlyLysTyThrCysGluGlyLysArgValArgTyArgSerCysAsn	592
DB	2160	GTCCCAAGAACCGAGGAGAGTACTGTGAAGGCAACAGCTCCGCTACAGTCTCTGTAAC	2219
QY	593	LeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHis	612
DB	2220	ATCGAGACTGTCCAGCAATAACCGAAACCTTCTAGAGGAGGAGTGTGCGAGGCGCAC	2279
QY	613	AsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTy	632
DB	2280	AATGAGTTTCCAAAGCTCTCTTTGGGAATGAGCCCACTGTAGAGTGGACACCAAGTAC	2339
QY	633	AlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTy	652
DB	2340	GCGGCGTCTCGCAAGGACAGTCCAAAGCTCACCTGTGAAGCCCAAGGATTTGGCTAC	2399
QY	653	PhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSer	672

Db 2400 TTTTTCGTCTTACAGCCCAAGGTGTAGATGGGACCTCCCTGTAGTCCAGACTTCACTCT 2459
Qy 673 ValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLys 692
Db 2460 GTCTGTGTCAAGGGCAGTGTGTGAAGCTGGCTGTGTGATCGCATATAGACTCCAAAAG 2519
Qy 693 LysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysLysSerGly 712
Db 2520 AAGTTTGAATGATGTGGCTTTGTGGAGNACGGTTCCACATGCAAGAGATGACAGA 2579
Qy 713 SerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThr 732
Db 2580 ATAGTCACTAGTACAAGACCTGGGTATCATGACATTTGTCACAAATCTCTGTGGAGCCAC 2639
Qy 733 AsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAla 752
Db 2640 AACATTGAAGTGAACATCGAATCAAGAGGGGTCCAGAAACAAATGGCAGCTTTCTGGCT 2699
Qy 753 IleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGlu 772
Db 2700 ATTAGAGCCGCTGATGATACCTATATCTGAATGGAAACTTCACTCTGTCCACACTAGAG 2759
Qy 773 GlnAspIleValThrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGlu 792
Db 2760 CRAAGCCTCACCTACAAAGGTACTGTCTTAAGGTACAGTGGTTCTCTCGCTCGCTGGAA 2819
Qy 793 ArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGly 812
Db 2820 AGAATCGCAGCTTTAGTCCACTCAAGAACCTTTAAACATCCAGTTCTTATGTGTAGGC 2879
Qy 813 AsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPhe 832
Db 2880 CATGCTCTCGACCCCAAAATTAATTCACCTACTTTATGAAGAAGAGAGGAGTCTCCAGACA 2939
Qy 833 AsnAlaIleProThrPheSerAlaTyrValIleGluGluThrGlyGluCysSerLysSer 852
Db 2940 AAGCCATTTCCCAATTTCTGAGTGGTGAATGAAAGAGGGGGAGTCTCCAGACA 2999
Qy 853 CysGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAla 872
Db 3000 TCGGGCTCAGTTGGCAGAGAGAGTAGTGCAGTGCAGAGACATTAACGGACACCCTGCT 3059
Qy 873 SerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 892
Db 3060 TCCGAATGTGCNAAAGGAAGTGAAGCCAGCCAGTACCAGACCTTGTGCAGACCTTCTCTGC 3119
Qy 893 ProGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLys 912
Db 3120 CCACACTGGCAGGTGGGGATTTGTCACCATGTTCNAAACTTCCGGGAAGGTTACAG 3179
Qy 913 LysArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAsp 932
Db 3180 AAGAGAACCTTGAATGTGTCTCCACGATGGGGGGTGTGTATCAATGAGAGCTGTGAT 3239
Qy 933 ProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
Db 3240 CCITTGAAGAGCCAAAGCAATTAATGATTTTGACACTGTACACAGTGCAGT 3293

RESULT 12

US-09-389-687-20
; Sequence 20, Application US/09989687
; Publication No. US2004000249A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4180

; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-989-687-20

Alignment Scores:
Pred. No.: 0 Length: 4180
Score: 4299.50 Matches: 789
Percent Similarity: 89.31% Conservative: 57
Best Local Similarity: 82.36% Mismatches: 97
Query Match: 82.86% Indels: 15
DB: 11 Gaps: 5

US-09-373-658C-2 (11-950) x US-09-989-687-20 (11-4180)
Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 441 ATGGGGGACGTCACAGCGGCGACGAGATCTCGGGGCTCTCTGTCGCGCACACATGCTGTG 500
Qy 21 LeuLeuAlaAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37
Db 501 CTGCTCTCCCTCCCTCCATACAAATGCTGTATGTGCGGGGGCGCACCGGGGCCCCACG 560
Qy 38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHisGly----- 55
Db 561 GAGGAAGATGAGAGCTGCTGCTCGCTCGAGCGCGCCCGCGCCCGCCACGATTCACCC 620
Qy 56 ThrThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAsp 75
Db 621 ACCACACGCTTCTGCTTGAGCGCTTTGGCAGCAGCTACATCTGAAGTTGGACGCGGAC 680
Qy 76 SerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGlu 95
Db 681 AGCGGTTCTTGGCGCTCGCTTACCTCCCTGCGAGCTGTGGGGCGCAGTCCCGGTCGAG 740
Qy 96 ThrProLeu-----ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsn 113
Db 741 GCACAACATCTCGACCCACCGGGGACCTGGCTCACTGCTTCTACTCTGGCAGGTGAAC 800
Qy 114 GlyAspProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyr 133
Db 801 GGTGATCCCGGCTCTGCGCGACCCCTCAGCCTCTGTGAAGGTGTGCTGTGCTCTTCTAC 860
Qy 134 LeuLeuGlyGluAlaTyrPheIleGlnProLeuPro-----AlaAlaSerGluArgLeuAla 152
Db 861 CTACAAGAGAGAGAGTCTTCTTCAATCAGCCCGCTGGAGTGGCCACCGAGCGCTGGCC 920
Qy 153 ThrAlaAlaProGlyGluLysProAlaProLeuGlnPheHisLeuLeuArgArgAsn 172
Db 921 CTGTCGTCGCGCGAGAGAGATCATCCGACCGCCGCGAGTTCACATCTCTGAGGGGAGG 980
Qy 173 ArgGlnGlyAspValGlyThrCysGlyValValAspAspGluProArgProThrGly 192
Db 981 CGCGGGGCGAGTGGCGGCGCCCAAGTGGCGGCTCATGACGCGCTGGAGTGGCCACCGCT 1037
Qy 193 LysAlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTyr 212
Db 1038 -----AGCGACTCGCGACCCGAGAGCCGAGAACACCGCGGACCGAGTGG 1079
Qy 213 SerProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArg 232
Db 1080 CCGTGTGCGGACCCCGCTCAGGACGCGGGGAAAGCCATCAGGACCGAGGAGGATAAGG 1139
Qy 233 LysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSer 252
Db 1140 AAGAAGCGAATTTGTGTCCAGCCCCCGTTATGTGGAACCATGCTCTAGTACGACGATCC 1199
Qy 253 MetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 272
Db 1200 ATGGCGGACTTCCACGGCAGCGGTCTAAGCATTTACTTTTAACTCTGTTCTCGGTGGCA 1259
Qy 273 AlaArgLeuTyrIleHisProSerIleArgAsnSerValSerLeuValValLysIle 292

;; TITLE OF INVENTION: Molecular Toxicology Modeling

;; FILE REFERENCE: 44921-5089-US

;; CURRENT APPLICATION NUMBER: US/10/152,319A

;; CURRENT FILING DATE: 2002-05-22

;; PRIOR APPLICATION NUMBER: US 60/292,335

;; PRIOR FILING DATE: 2001-05-22

;; PRIOR APPLICATION NUMBER: US 60/297,523

;; PRIOR FILING DATE: 2001-06-13

;; PRIOR APPLICATION NUMBER: US 60/298,925

;; PRIOR FILING DATE: 2001-06-19

;; PRIOR APPLICATION NUMBER: US 60/303,810

;; PRIOR FILING DATE: 2001-07-10

;; PRIOR APPLICATION NUMBER: US 60/303,807

;; PRIOR FILING DATE: 2001-07-10

;; PRIOR APPLICATION NUMBER: US 60/303,808

;; PRIOR FILING DATE: 2001-07-10

;; PRIOR APPLICATION NUMBER: US 60/315,047

;; PRIOR FILING DATE: 2001-08-28

;; PRIOR APPLICATION NUMBER: US 60/324,928

;; PRIOR FILING DATE: 2001-09-27

;; PRIOR APPLICATION NUMBER: US 60/330,867

;; PRIOR FILING DATE: 2001-11-01

;; PRIOR APPLICATION NUMBER: US 60/330,462

;; PRIOR FILING DATE: 2001-10-22

;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 2221

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 1840

;; LENGTH: 4878

;; TYPE: DNA

;; ORGANISM: Rattus norvegicus

;; FEATURE:

;; OTHER INFORMATION: Genbank Accession No. NM_024400

US-10-152-319A-1840

Alignment Scores:

Pred. No.: 0 Length: 4878

Score: 4292.00

Percent Similarity: 88.40%

Best Local Similarity: 82.45%

Query Match: 82.71%

DB: 12

US-09-373-658c-2 (1-950) x US-10-152-319A-1840 (1-4878)

QY 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20

DB 446 ATGGGGGACATCCAGCGGGCAGCGAAGTTTCGGAGCTCTCAGCTCCACACATGCTGTTG 505

QY 21 LeuLeuAlaAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37

DB 506 CTACTCTCGCTTCCATAACAATGCTGTGTGCGGGGCGCCACACGCGGCGCCACG 565

QY 38 GluGluAspGluGluLeuValProGluLeuGluArgAlaProGlyHis---GlyThr 56

DB 566 GAGGAAGACAGAGAGCTGTGTGCTGCTCGCTGAGCGCGCGCGGCGCCAGATTCCACC 625

QY 57 ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGluLeuArgProAspSer 76

DB 626 ACACTCTCGCTGAGCGCTTGTGTGTCAGCAGCTGCTTGAAGTTGCGAGCGACAGC 685

QY 77 SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThr 96

DB 686 GGTTCCTTAGCGCTTTCACCCCTCCAGACCGGTGGCGGCGAGTCTGCGTCCGAGGCA 745

QY 97 ProLeu-----ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGly 114

DB 746 CAGCATCTGAGACCCACTGGGGACCTGGCCACTGCTTCTACTCTGGCAGCGTGAACGT 805

QY 115 AspProSerSerAlaAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeu 134

DB 806 GACCCGAGCTCCCGCCCGCCCTCAGCCTCTGGAAGGTGTGCGCGTGCCTTCTACCTA 865

QY 135 LeuGlyGluAlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThr 153

DB 866 CAAGCGGAGGAGTTCATTTCAGCCAGCGCTGGGTGGCCACCGAGGCTGTGTCCCC 925

QY 154 AlaAlaProGlyGluLeuProAlaProLeuGlnPheHisLeuLeuArgArgSerArg 173

DB 926 GCCGAACCGAAGGAGGAGTCAATCCGCGTTCACATCTCTGAGGCGAAGGCGG 985

QY 174 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 193

DB 986 CGGGGACCGCGCGCGCAAGTGGGTGTATGAGACGAAGAGACCCCTGCCAACCC 1039

QY 194 AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer 213

DB 1040 -----AGCAACTCGGTCGCGAAGCCAGACACACCCCGAGCAGTGGCT 1084

QY 214 ProGlnAspProAlaLeuGlnGlyValGlnProThrGlyThrGlySerIleArgLys 233

DB 1085 CTGCGGAACCCCACTCTCAGGCGCGGGAAGCCACAGGACCGAGGAGCATAGGAAG 1144

QY 234 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 253

DB 1145 AAGCGATTGTGTCCAGCCCGCGTTATGTGGAACCATGCTGTGGCTGACCATCATG 1204

QY 254 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAla 273

DB 1205 GCTGACTTCCACGCGGCGGTCTAAGCAATTACCTTCTAACCTGTTCTCGGTGGAGCC 1264

QY 274 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu 293

DB 1265 AGATTTHACAGCACCCAGCATTAAGGAATTCATTAGTCTGTGTGTGTGGAAGATCTTG 1324

QY 294 ValIleHisAspGluGlnLysGlyProGluValThrSerAspAlaAlaLeuThrLeuArg 313

DB 1325 GTCATATATGAGGACGAGAGGACCGGAAGTTACTTCCAAATGCGGCTCTCACCTTAGG 1384

QY 314 AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 333

DB 1385 AATTTCCTGTGTGTCGAGAAACAGCACACAGCCCGAGTGACCGGATCCAGAGCACTAT 1444

QY 334 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 353

DB 1445 GACACAGCGATTCTGTTCCACACAGACAGGATTTATGTGGCTCCACACACCTGTGACACTC 1504

QY 354 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 373

DB 1505 GGGATGGCTGATGTGTGAAGTATGTGACCCCGACGAGAGCTGTTCGGTCAATCGAAGAT 1564

QY 374 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro 393

DB 1565 GATGTTTACAGGCTGCTTCCACACAGCCCATGAATTTGGGCCATGTGTTTAACATGCCA 1624

QY 394 HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 413

DB 1625 CACGATGACGCCAACGACCTGCGCCAGCTTTAATGCGGTGAGTGGGATTTCCCATCTGATG 1684

QY 414 AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet 433

DB 1685 GGCTCGATGCTCTCCAGCTTGACCCACAGCCAGCCCTGGTCTCTCTTGCAGTCCCTACATG 1744

QY 434 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 453

DB 1745 GTCATCATCTCTGACAAACGCGCATGGGAATTTGATGGACAAAGCCGAGACCCCA 1804

QY 454 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 473

DB 1805 ATCAGCTCCCATCTGATCTTCCCGGTACCTTGTAGATGCGCAACCGCCAGTGTCACTTT 1864

QY 474 ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp 493

DB 1865 ACCTTCGGGGAGGAATCCACGCACTGCTGTATGTCAGCCAGCACATGACATACCTGTGG 1924

QY 494 CysThrGlyThrSerGlyValLeuValCysGlnThrLysHisPheProTrpAlaAsp 513

Db 1925 TGCACTGGCACCTCGGTGGCTTACTGGTGTGCCAAACAAACACTTCCCTTGGGCAGAT 1984
Qy 514 GlyThrSerCysGlyGluGlyValThrCysIleAsnGlyLysCysValAsnLysThrAsp 533
Db 1985 GGACACGAGCTGGGAGAGGAAATGGTGTGTGAGGCGCAAGTGTGTGACACAGACCGAC 2044
Qy 534 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp 553
Db 2045 ATGAAGACACTTGTCTACTCTGCTTCTATGGGAGCTGGGACCGCTGGGGACCAATGGGGAGAC 2104
Qy 554 CysSerArgThrCysGlyGlyValGlnThrMetArgGlyCysAspAsnProVal 573
Db 2105 TGCTCAAGAACCTGTGTGGAGAGTTCATATACATGAGAGCAATGTGACACCCCGGTG 2164
Qy 574 ProLysAsnGlyGlyLysThrCysGluGlyLysArgValArgGlyArgSerCysAsnLeu 593
Db 2165 CCAAGAGACGGGGGAAGTACTCGGAAGGCAACAGTCCGCTACAGGTCTCTGTAAACATT 2224
Qy 594 GluAspCysProAspAsnAsnGlyLysThrPheArgGlyGluGluLysCysGluAlaHisLeu 613
Db 2225 GAGGACTGTCCAGACAAATAACGGAAACAAATTCAGAGGAGCAATGCGAGGCGCACAAAT 2284
Qy 614 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysThrAla 633
Db 2285 GAGTTTTCACAGCTTCCITTCGGAATGAACCCAGCGTGGATGGACACCCCAAGTATGCT 2344
Qy 634 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyThrPhe 653
Db 2345 GCGGTCTGCCAAAGACAGGTGCAAGCTTACTCTCGAAGCCAAAGGCAATGGCTACTTTC 2404
Qy 654 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 673
Db 2405 TTTGTTTACACCCCAAGGTGTAGTGGCACTCCCTGTAGTCCAGACTCTACTTCTGTC 2464
Qy 674 CysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 693
Db 2465 TGTGTGCAAGGACAGTGTGTGAAGCTGCTGTGATCGCATCATAGACTCCAAAAGAGAG 2524
Qy 694 PheAspLysCysGlyValCysGlyGlyValAsnGlySerThrCysLysValIleSerGlySer 713
Db 2525 TTCGATAGTGTGGGTGTGGAGGAATGCTCCAGTGCAGAAATATTCAGGAACG 2584
Qy 714 ValThrSerAlaLysProGlyThrHisAspIleIleThrIleProThrGlyAlaThrAsn 733
Db 2585 GTCACTAGTACCAAGCTGGGTATCATGACATTTGTACAAATTCCTGCTGGAGCCCAAC 2644
Qy 734 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheIleAlaIle 753
Db 2645 ATTGAAGTGAAACATCGTATCCAAAGGGGATCCAGAAACAATGGCAGCTTTCTGCTATT 2704
Qy 754 LysAlaAlaAspGlyThrTyrlleLeuAsnGlyAspTyrlleGlnValLeuThrLeuGluGln 773
Db 2705 AGAGCTGCAGATGGTACCTATATTCTGAATGGAACCTTCACTCTGTCCACTCTAGAGCAA 2764
Qy 774 AspIleMetTyrlleGlyValValleuArgTyrlleSerGlySerSerAlaAlaLeuGluArg 793
Db 2765 GACCTCACCTCAAAAGGACTGTCTTAAGATACAGTGTCTCTCAGCAGCATTTGAAGA 2824
Qy 794 IleArgSerPheSerProLysGluProLeuThrIleGlnValLeuThrValGlyAsn 813
Db 2825 ATCCGAGCTTTAGTCCACTCAAGAACCCCTGACCATCCAGTCTTATGTGGGCCAT 2884
Qy 814 AlaLeuArgProLysIleLysTyrlleThrTyrllePheValLysLysLysGlySerPheAsn 833
Db 2885 GCTCTCCGACCCAAATAAAGTACACCTATTATTATGAAGAGAAAGACGGGCGCTTCAAC 2944
Qy 834 AlaIleProThrPheSerAlaTrpIleGluGluTrpGlyGluCysSerLysSerCys 853
Db 2945 GCTATTCCRCATTTTCGAGTGGGTGATTTGAAGAGTGGGGGAGTGTCTCCAGGCATGT 3004
Qy 854 GluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSer 873

Db 3005 GGTTCCTGGTGGCAGAGAGAGTGGTAGAGTGCAGAGACATTAATGACACCCCTGCTCT 3064
Qy 874 GluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPro 893
Db 3065 GAATGTGCCAAAGAGTGAAGCCAGCCAGTACACAGACTTGTGCGAGACCTTCTTGTGCCCA 3124
Qy 894 GlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyLysGlyLys 913
Db 3125 CGTTGGCAGGTGGGGGATGTGTCCACATGTTCTAAACTTGTGGGAAGGTTAAGAAG 3184
Qy 914 ArgSerLeuLysCysLeuSerHisAspGlyValLeuSerHisGluSerCysAspPro 933
Db 3185 AGAACCTTGAATGCTGTCCCATGATGGCGTGTGTATCATATGAGAGCTGTGTATCT 3244
Qy 934 LeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 950
Db 3245 TTGAAGAAACCAAGCAATTAATGACTTTTGCATCTATGACACAGTGCAGT 3295
RESULT 14
US-10-191-803-170
; Sequence 170, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191.803
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_024400
US-10-191-803-170
Alignment Scores:
Pred. No.: 0 Length: 4878
Score: 4292.00 Matches: 789
Percent Similarity: 88.40% Conservative: 57
Best Local Similarity: 82.45% Mismatches: 97
Query Match: 82.71% Indels: 14
DB: 16 Gaps: 5
US-09-373-658C-2 (1-950) x US-10-191-803-170 (1-4878)
Qy 1 MetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeu 20
Db 446 ATGGGGACATCCAGCGGAGCGAGAGTTCGGAGCTCTCAGTCTGCACACATCTGTGTG 505
Qy 21 LeuLeuAlaAlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSer 37
Db 506 CTACTCTCGTCTCCATAACAATGCTGTGTGTGGGGGCGCACACGCGCGCCCCACG 565
Qy 38 GluGluAspGluGluLeuValValProGluLeuGluArgAlaProGlyHis---GlyThr 56
Db 566 GAGGACACGAGAGCTGGTGTCTGCTCGCTCGTGTGAGCGCGCCCGGCCACGATTCRCC 625

Qy	57	ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuGlnLeuArgProAspSer	76
Db	626	ACACTCTCGTCTGGACGCGCTTTGGTTCACGACGCTGCATCTGAAGTTGCGACGACAGC	685
Qy	77	SerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerGluThr	96
Db	686	GGTTTCTTAGCGCTGGCTTACCTCCACACGTCGGTGGGCGCAGTCTTGGGTCCGAGGCA	745
Qy	97	ProLeu-----ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGly	114
Db	746	CAGCATCTGGACCCACTGGGGGACCTGGCCCACTGCTTCTACTCTGGCACGGTGAACGGT	805
Qy	115	AspProSerSerAlaAlaAlaLeuSerLeuCysGluCluLlyValArgGlyAlaPheTyrLeu	134
Db	806	GACCCACAGCTCCGCGCGCGCCCTCAGCCTCTGTGAAGGTGTGCGGTGCTCTTACCTA	865
Qy	135	LeuGlyGluAlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThr	153
Db	866	CAAGGCGAGGAGTTCTTCATTACGACAGCGCTTGGGTGGCCACCGAGCGCTTGGTCCCC	925
Qy	154	AlaAlaProGlyGlnLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArg	173
Db	926	GCCGAACCGAAGGAGGAGTCAATCGCACCTTCGCGGTTCACATCTCTGAGCGCAAGCGG	985
Qy	174	GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys	193
Db	986	CGGGCAGCGCGCGCAAGTGGGTGTTCATGACGACGAGAGCCCTGCCCAAC-----	1039
Qy	194	AlaGluThrGluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSer	213
Db	1040	-----ACCAACTCGGGTCGCGAAGCCAGACACCCCGGACCCAGTGGCCT	1084
Qy	214	ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys	233
Db	1085	CTGGGAACCCCACTCTCTAGGGCGCGGAAAGCCACACAGGACAGGAGCATAAGGAAG	1144
Qy	234	LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet	253
Db	1145	AAGCGATTGTGTCCAGCCCGGTATGTGGAACCACTGTCGTGGTGACCACTCCATG	1204
Qy	254	AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla	273
Db	1205	GCTCATTTCCACGGCAGCGGTCTAAGACATTACTTCTAACCTTGTTCTCGTGGCAGCC	1264
Qy	274	ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu	293
Db	1265	AGATTTTACAGCACCCCGACATTAGGAATTCAAATAGTCTGGTGGTGGTGAAGATCTTG	1324
Qy	294	ValIleHisaspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg	313
Db	1325	GTCATATATGAGGACGAGAAGGACCGGAAGTTACTTCCAAATGCGGTCTCACCCCTTAGG	1384
Qy	314	AsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr	333
Db	1385	AATTTCTGTAGCTGCGAGAAACAGCAACACGCCCGGATCCAGGATCCAGAGCACTAT	1444
Qy	334	AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu	353
Db	1445	GACACAGCGATTCTGTTTACACAGACAGATTATGTGCTCTCCACACTGTGACACTCTC	1504
Qy	354	GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp	373
Db	1505	GGGATGCTGATGTTGGNACTGTATGTACCCCGGACGAGGAGCTGTTCGGTTCATCGAAGAT	1564
Qy	374	AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetPro	393
Db	1565	GATGGTTTACAGGCTGGCTTCACACAGCCCATGAATGGGCCCATGTGTTTAAACATGCCA	1624
Qy	394	HisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet	413
Db	1625	CACGATGACGCCAAGCACTCGCCAGCTTTTAATGGGTGAGTGGGGATTCACACTGATG	1684
Qy	414	AlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerAlaTyrMet	433

Db	1685	GCCTCGATGCTCTCCAGCTTGGACCAACAGCCGCTTGGTCTCTCTGTCAGTGGCTACATG	1744
Qy	434	ILeThrSerPheLeuAspAenGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro	453
Db	1745	GTCACATATCTCTGTGACCAACGGCCATGGGGAATGTTTGATGACCAAGCCGACAGACCCA	1804
Qy	454	ILeGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe	473
Db	1805	ATCAAGCTCCCACTGATCTCTCCGGTACCTGTACAGTCCCAACCCAGTGTCACTTT	1864
Qy	474	ThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrp	493
Db	1865	ACCTTCGGGAGGAATCCAGCACTGCCCTGTGATGCAGCCAGCACATGCATCACTCTGTGG	1924
Qy	494	CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAsp	513
Db	1925	TGCACTGGCACTCCGGTGGCTTACTCGTGTGCGAAACAAACACTTCCCTTGGGCAGAT	1984
Qy	514	GlyThrSerCysGlyGluGlyLysTrpCysILEAsnGlyLysCysValAsnLysThrAsp	533
Db	1985	GGCACCAAGCTCCGAGAAAGGAAATGGTGTGTCAGCGCAAGTGTGTGAAACAAGACCGAC	2044
Qy	534	ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAsp	553
Db	2045	ATGAAGCACATTGCTACTCTCTGTTTCATGGAGCTGGGACCGTGGAGAACCATGGGGAGAC	2104
Qy	554	CysSerArgThrCysGlyGlyValGlnTyrThrMetArgLysCysAspAsnProVal	573
Db	2105	TGCTCAAGAACCCTGTGTGGAGGAGTTCATATATACATGAGAGAATGTGCAACCCGGCT	2164
Qy	574	ProLysAsnGlyLysTyrCysGluGlyValArgValArgTyrArgSerCysAsnLeu	593
Db	2165	CCAAAGAACCGGGGAAGTACTCGAAGGCAACGAGTCCGCTACAGGTCTCTGTACATT	2224
Qy	594	GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn	613
Db	2225	GAGACTGTCCAGACATACCGGAAAACATTTCAGAGAGGAGCAATCGAGGGCGCAAT	2284
Qy	614	GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpLleProLysTyrAla	633
Db	2285	GAGTTTTCCAAAGCTTCTCTTTGGGAATGAACCCACGCTGGAATGGACACCAAGATGCT	2344
Qy	634	GlyValSerProLysAspArgCysLysLeuLleCysGlnAlaLysGlyLleGlyTyrPhe	653
Db	2345	GGCGTCTCGCCAAAGGACAGGTGCAGCTTACCTGCGAAGCCAAAGSCAATTGGCTACTTC	2404
Qy	654	PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal	673
Db	2405	TTTTGTTTTACAGCCCAAGTGGTAGATGGCACTCCCTGTAGTCAGACTCTACTCTGTCT	2464
Qy	674	CysValGlnGlyGlnCysValLeuAlaGlyCysAspArgLlelleAspSerLysLysLys	693
Db	2465	TGTTGCAAGGACAGTGTGTGAAGCTGGCTGTGTATCGATCATAGACTCCAAAAGAGAG	2524
Qy	694	PheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysLleSerGlySer	713
Db	2525	TTTCATTAAGTGTGGCGTTTGTGGAGGAAATGGCTCCACGTCGAAGAAAATATACGGAACG	2584
Qy	714	ValThrSerAlaLysProGlyTyrHisAsnLleThrIleProThrGlyAlaThrAsn	733
Db	2585	GTCACTAGTACAGACCTGGGTATCATGACATGTTGTCAATTCCTCTGGAGCCACCAAC	2644
Qy	734	IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaLle	753
Db	2645	ATTGAATGTAACATCATGTAATCCAAAGGGATCCAGAAACCAATGGCAGCTTCTGGCTATT	2704
Qy	754	LysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln	773
Db	2705	AGAGCTGCAGATGGTACTATATTCTGAATGGAACCTTCATCTGTCCACTCTAGAGCAA	2764
Qy	774	AspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg	793

Db 2765 GACCTCACCTACAAAGGTAAGTCTCTTAAGATACAGTGGTCTCTCAGCAGCAATGGAAAGA 2824
Qy 794 IleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsn 813
Db 2825 ATCCGACACTTATGTCACCTCAAGAACCCCTGACCATCCAGGTTCTTATGTTGGCCAT 2884
Qy 814 AlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysLysLysPheAsn 833
Db 2885 GCTCTCCAGCCCAAAATCAAGTACACCTATTTTATGTAAGAAAGAAAGACGAGCCCTTCAAC 2944
Qy 834 AlaIleProThrPheSerAlaIleValIleGluGluTyrGlyGluCysSerLysSerCys 853
Db 2945 GCTATTCACATTTTCGAGTGGGTGATTGAGAGTGGGGGAGTGTCCAGACATGT 3004
Qy 854 GluLeuGlyTyrPheArgLeuValGluCysArgAspIleAsnGlyGlnProLaser 873
Db 3005 GGTTCGGTGGCAGAGAGTGGTAGAGTGCAGAGACATTAATGAGACACCCCTGCTTCT 3064
Qy 874 GluCysAlaLysGluValLysProLaserThrArgProCysAlaAspHisProCysPro 893
Db 3065 GAATGTGCAAGAAAGTGAAGCAGCCAGTACCAGACTTGTGAGACCTTCCTTGCCCA 3124
Qy 894 GlnTrpGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 913
Db 3125 CGTTGGCAGGTGGGGGATGGTCCACATGTTCTTAAATCTTGTGGGAGGGTTATAAGAAG 3184
Qy 914 ArgSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisGluSerCysAspPro 933
Db 3185 AGAACCCTTGAATGCTGTGCCATGATGGCGGTGTATCAATGAGAGCTGTGATCCT 3244
Qy 934 LeuLysLysProLysPheIleAspPheCysThrMetAlaGluCysSer 950
Db 3245 TTGAAGAAACCAAGACATTACATTCATCTTTGTCATCTGACACAGTGCAGT 3295

RESULT 15

US-09-445-023A-2
; Sequence 2, Application US/09445023A
; Patent No. US20020119167A1
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Biiji
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioaka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: QS7092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-150422
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:
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Score: 3947.00 Matches: 712
Percent Similarity: 99.44% Conservative: 4
Best Local Similarity: 98.89% Mismatches: 4
Query Match: 76.06% Indels: 0
DB: 9 Gaps: 0

US-09-373-658C-2 (1-950) x US-09-445-023A-2 (1-2184)

Qy 231 IleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAsp 250
Db 22 CTTAGGAAGAAGCGATTGTGTCCAGCCCCCGTTATGTGGAAACCATGCTGTGTGGCAGAC 81
Qy 251 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 270
Db 82 CAGTCGATGCGAGATTCACAGCAGTGGTCTAAAGCATTAACCTTCTCAGCTGTGTTTCG 141
Qy 271 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 290
Db 142 GTGGCAGCCAGATTGTACAAACACCCCGAGCATTCGTAATTCAGTTAGCTGGTGGTGGT 201
Qy 291 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 310
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Qy 311 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 330
Db 262 ACTCTCGGAACCTTTTCCAACTGCGACAGACAGCACCAACCCACCTAGTACCCTGGATGCA 321
Qy 331 GluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCys 350
Db 322 GAGCATATGACACAGCAATTCCTTTTCCACAGACAGGACTTGTGTGGTCCACAGCATGT 381
Qy 351 AspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerVal 370
Db 382 GATACTCTTGGGATGGCTGATGTTGGAACCTGTGTGTATCCGACAGAGCTGCTCCGTC 441
Qy 371 IleGluAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhe 390
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Db 502 AACATGCCACATGATGATGCAAGACAGTGTGCCAGCTTAATGTGTGAACACAGGATTC 561
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Db 562 CACATGATGGCGTCAATGCTTCCAACTGACACACAGCAGCCCTTGGTCTCTCTGTCAGT 621
Qy 431 AlaTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysPro 450
Db 622 GCCTACATGATTACATCATTTCTGGATATGGTCACTGGGAATGTTTGTATGACAGCCT 681
Qy 451 GlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGln 470
Db 682 CAGAAATCCCATACAGCTCCAGGCGATCTCCCTGGCACCTTGTACGATGCCAACCGGCGAG 741
Qy 471 CysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 490
Db 742 TCCAGATTTACATTTGGGAGGAGTCCAAACACTGCCCCCGATGCGAGCAGCATGTAGC 801
Qy 491 ThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPhePro 510
Db 802 ACCTTGTGGTACCGGCACCTCTGTGTGGGTGTGTGGTGTGTCAAAACCAACACACTTCCG 861
Qy 511 TrpAlaAspGlyThrSerCysGlyGluGlyValLeuValLeuValLeuValLeuValLeu 530
Db 862 TGGGCGGATGGCAGCAGCTGTGGAGAGGGGAATGGTGTATCAACGCGCAAGTGTGTGAC 921
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Job time : 1093.17 secs

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Qy 671 ThrSerValCysValGlnGlnCysValLysAlaGlyCysAspArgIleLeuAspSer 690
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Qy 711 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 730
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Qy 731 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 750
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Qy 771 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 790
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Qy 831 SerPheAsnAlaIleProThrPheSerAlaTyrValIleGluIleGluTyrGlyGluCysSer 850
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GenCore version 5.1.6
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Run on: June 18, 2004, 17:11:45 ; Search time 150.321 Seconds
(without alignments)
3569.936 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	99.0	4676	US-09-130-491-1	Sequence 1, Appli
2	5230	98.9	3889	US-09-568-559-1	Sequence 1, Appli
3	5219	98.7	4858	US-09-392-184-1	Sequence 1, Appli
4	4262	80.6	3706	US-09-484-9703-58	Sequence 58, Appli
5	3922	74.2	2184	US-09-445-023A-2	Sequence 2, Appli
6	3652	69.1	2184	US-09-445-023A-13	Sequence 13, Appli
7	2271.5	43.0	3638	US-09-369-364A-8	Sequence 8, Appli
8	2165	40.9	3126	US-09-392-184-7	Sequence 7, Appli
9	2156	40.8	4192	US-09-122-126B-1	Sequence 1, Appli
10	2156	40.8	4192	US-09-634-286A-1	Sequence 1, Appli
11	1926.5	36.4	3250	US-09-122-126B-14	Sequence 14, Appli
12	1926.5	36.4	3250	US-09-634-286A-14	Sequence 14, Appli

13	1909.5	36.1	3002	4	US-09-369-364A-1	Sequence 1, Appli
14	1751.5	33.1	5804	4	US-09-369-364A-12	Sequence 12, Appli
15	1613	30.5	2625	4	US-09-369-364A-14	Sequence 14, Appli
16	1406	26.6	2114	4	US-09-130-491-7	Sequence 7, Appli
17	1333.5	25.2	5357	4	US-09-392-184-5	Sequence 5, Appli
18	1278.5	24.2	3675	4	US-09-930-872-3	Sequence 3, Appli
19	1278.5	24.2	4042	4	US-09-930-872-5	Sequence 5, Appli
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21	1214.5	23.0	2727	4	US-09-963-791-1	Sequence 1, Appli
22	1203	22.8	3885	4	US-09-369-364A-16	Sequence 16, Appli
23	1151.5	21.8	2274	4	US-09-963-791-23	Sequence 23, Appli
24	1112	21.0	6892	4	US-09-491-522-1	Sequence 1, Appli
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26	1066.5	20.2	3160	4	US-09-963-791-25	Sequence 25, Appli
27	1040.5	19.7	1520	4	US-09-369-364A-3	Sequence 3, Appli
28	1038.5	19.6	2848	4	US-09-369-364A-4	Sequence 4, Appli
29	950.5	18.0	2450	4	US-09-491-522-2	Sequence 2, Appli
30	949.5	18.0	2450	4	US-09-491-522-9	Sequence 9, Appli
31	781	14.8	1770	4	US-09-963-791-11	Sequence 11, Appli
32	718	13.6	1317	4	US-09-963-791-21	Sequence 21, Appli
33	712.5	13.5	739	4	US-09-369-364A-10	Sequence 10, Appli
34	639	12.1	1810	4	US-09-833-381-1056	Sequence 1056, Ap
35	607.5	11.5	703	4	US-09-392-184-6	Sequence 6, Appli
36	595	11.3	5720	4	US-09-800-729-18	Sequence 18, Appli
37	593.5	11.2	1524	4	US-09-963-791-9	Sequence 9, Appli
38	568.5	10.8	1803	4	US-09-369-364A-20	Sequence 20, Appli
39	530.5	10.0	1071	4	US-09-963-791-19	Sequence 19, Appli
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41	492	9.3	2023	4	US-09-491-522-6	Sequence 6, Appli
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44	436	8.2	954	4	US-09-963-791-15	Sequence 15, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Goodgearl, Douglas A.
; APPLICANT: Holtzman, Andrew D. J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
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Pred. No.: 0
Score: 5232.00
Percent Similarity: 99.98%
Best local similarity: 98.97%
Query Match: 98.96%
DB: 4
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Matches: 957
Conservative: 4
Mismatch: 6
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US-09-373-658C-126 (1-967) x US-09-130-491-1 (1-4676)

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DB 760 AGCTCCAGAACGTCGGGCGCAATCCGGTCCGAGACCGCGCTTCCGGAACCGACCTG 819
QY 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 820 GCGCATGCTTCTACTCCCGGACCGTGAATGGCGATCCAGCTCGGCTCGCCGCCCTCAGC 879
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QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLeuProProAlaPro 180
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QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPhePheHisGly 560
DB 2080 ATCAACGCGAGTGTGTGAACAAAACCGACAGAAAGCATTTTCATACGCTTTTCATGA 2139
QY 561 SerTyrGlyMetTyrProGlyProGlyAspCysSerArgThrCysGlyGlyValGln 580
DB 2140 AGCTGGGAAATGTGGGGCGCTTGGGAGACTGTTCGAGAACGTCGGTGGAGAGTCCAG 2199
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
DB 2200 TACAGTATGAGGAATGTGTCAACCCAGTCCCAAGAAATGAGGAGAGTACTGTGAAGC 2259
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 2260 AAACGAGTGGCTACAGATCTCTTAACCTTGAAGACTGTCCAGACAATAATGGAATAACC 2319
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2320 TTTAGAGAGAACAAATGTGAGCACACACAGTCTTCAANAGCTTCTTTGGAGTGGG 2379
QY 641 ProAlaValGluTyrPheProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2380 CCGTGGGTGAAATGGATTCCAAGTACGCTGGCGCTCTCACAAAGGACAGGTGCAAGCTC 2439
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2440 ATTGCGCAAGCCAAAGCATTTGGCTACTTCTCGTTTTCGAGCCCAAGGTGTAGATGG 2499
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
DB 2500 ACTCCATGTAGCCAGATTCACCTCTGTGTGTGCAAGGACAGTGTGTAAAGCTGT 2559
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2560 TGTGATGCGCATCATAGACTCCAAAGAAAGATTTGATTAATGTGTGTGTTCGCGGGGAAAT 2619
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740

Db 2620 GGATCTACTTGTAAAAAATATACGGATCAGTTACTAGTCGCAAAACCTGGATATCATGAT 2679
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValIysGlnArgAsnGlnArgGly 760
Db 2680 ATCATCAATTCACATCGAGCACCACATCGAGTGAACAGCGGAAACAGAGAGGGA 2739
Qy 761 SerArgAsnGlySerPheLeuAlaIleIysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2740 TCAGGAACAAATGGCAGCTTCTTGCCATCAAGCTGCTGATGGCANTATATCTTAAT 2799
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrIysGlyValValLeuArg 800
Db 2800 GGTGACTACACTTGTCCACTTAGAGCAGAGACATATGTACAAAGGTGTGTCTTGAGG 2859
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuIysGluPro 820
Db 2860 TACAGCGGCTCTCTCGCGCATTTGGAAAGAAATTCGCAGCTTTAGCCCTCTCAAAAGAGCCC 2919
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProIysIleIysTyrThrTyr 840
Db 2920 TTGACCATCCAGGTTCTTACTGTGGGCATGTCCCTTCGACCTAAATTAATATACACTAC 2979
Qy 841 PheValIysIysIysIysGluSerPheAsnAlaIleProThrPheSerAlaIleProValIle 860
Db 2980 TTCGTAAAGAAAGAAAGAAATCTTCAATGTCTATCCCACTTTTTCAGCATGGGTCAAT 3039
Qy 861 GluGluTrpGlyGluCysSerIysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3040 GAAGAGTGGGGCGAAATGTTCTTAAGTCATGGAATTTGGGTGTGGCAGAGAGACTGGTAGAA 3099
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaIysGluValIysProAlaSer 900
Db 3100 TGGCGAGACATTAATGACAGCCCTGCTTCGAGTGTGCAAAAGAGTGAAGCCAGCCAGC 3159
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3160 ACCAGACCTTTGTGCAGACCATCTCCCTGCCAGTGGCAGCTGGGGAGTGGTCAATGAT 3219
Qy 921 SerIysThrCysGlyIysGlyTyrIysLysThrSertLeuIysCysLeuSerHisAspGly 940
Db 3220 TCTAAGACCTGTGGAGGGTTACAAAAAGAGAGCTTGAAGTGTCTGTCTCCCATGATGA 3279
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuIysIysProIysHisPheIleAspPhe 960
Db 3280 GGGGTGTATTCTCATGAGCTGTGATCTTTAAAGAAACCTAAACATTTTCATAGACTTT 3339
Qy 961 CysThrMetAlaGluCysSer 967
Db 3340 TGCACAAATGGCAATGCACT 3360

RESULT 2

US-09-568-559-1
; Sequence i, Application US/09568559
; Patent No. 6549377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrucanase and Nucleic Acid
; FILE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3889
; TYPE: DNA
; ORGANISM: human
US-09-568-559-1

Alignment Scores:

Pred. No.: 0 Length: 3889
Score: 5230.00 Matches: 956
Percent Similarity: 99.38% Conservative: 5
Best Local Similarity: 98.86% Mismatches: 6
Query Match: 98.92% Indels: 0
DB: 4 Gaps: 0
US-09-373-658c-126 (1-967) x US-09-568-559-1 (1-3889)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyA-GAtgLyLeuGlySerAspMetGlyVal 20
Db 8 ATGCAGCATCTGTCCCGAGGGTTCGAGAGGCGCAAGCTGGCAGCAGCATCGGGAAC 67
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 68 GCGAGCGGCGCTCGGGGTCTCGAGCTTTGGGCGCGTACCCACGCTGCTGCTGCTCGCC 127
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 128 GCGGCGCTACTGCGCGTGTGGAGCGCATCTCGGGCGCCCTCCGAGGAGGAGGAGCTA 187
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrArgLeuArgLeuHisAla 80
Db 188 GTGGTGGCGAGCTGGAGCGCGCCCGGAGCACAGGACACCGCGCTCGGCTCGCACGCC 247
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 248 TTGACCCAGCAGCTGGATCTGGAGCTGGCGCCCGCAGCAGCAGCTTTTGGCGCCCGGCTTC 307
Qy 101 ThrLeuGlnAsnValGlyArgIysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 308 ACCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGAGCGCGCTTCGGAACCGACCTG 367
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 368 GCGCATCTGTTCTACTCCGGCACCTGTAATGGCATGCCAGCTCGGCTCGGCTCGGCTCGC 427
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 428 CTCTGCGAGGGGTGGCGGCGCTTCTACTGCTGGGGAGGCGGTATTTTCATCCAGCG 487
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluIysProProAlaPro 180
Db 488 CTGCGCGCGCCGAGGAGCGCTCGCCACCGCGCCCGAGGAGAGCGCGCGGAGCGGCGG 547
Qy 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
Db 548 CTACAGTTCCACTCTCTGCGCGGGAATCGGAGGGGCGAGCTCGGCGGCGAGTGGGGGTC 607
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGlyThr 220
Db 608 GTGGACGACGAGCCCGCGCGCTGGGAAAGCGGAGACCGAAGACGAGGAGCGAGCT 667
Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaIleGluValGly 240
Db 668 GAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 727
Qy 241 GlnProThrGlyThrGlySerIleArgIysLysArgPheValSerSerHisArgTyrVal 260
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Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuIysHis 280
Db 788 GAAACCATGCTTGTGGCAGACAGCTCGATGGCAGAAATTCACCGGAGTGGTCTAAAGCAT 847
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrIysHisProSerIleArgAsn 300
Db 848 TACCTTCTCAGCTTGTTCGTGGCAGCCAGATTTGTACAAACACCCCGAGCATTCGTAA 907
Qy 301 SerValSerLeuValValIysIleLeuValIleHisAspGluGlnIysGlyProGlu 320

908 TCAGTTAGCTGGTGGTGAAGATCTTGGTTCATCCACGATGAACAGAGGGCGCGAA 967
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnHisAsn 340
968 GTGACCTCCAACTGCTCCCTCACTCTGCGGAACCTTTTGCAACTGGCAGAGCAGACAAC 1027
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaAlaLeuPheThrArgGlnAsp 360
1028 CCACCCAGTGCACCGGATGCAGAGCACTATGACACAGCAATCTTTTCCACGACAGGAC 1087
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
1088 TTGTGTGGGFPCCAGACATGTGATCTCTGGGATGGCTGATGTTGGAACTGTGTGTGAT 1147
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
1148 CCGAGCAGAGCTGCTCCGTCATAGAGATGATGGTTTACAGCTGCTTCCACGAGCC 1207
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
1208 CATGAATTAGCCACCTGTTTAAACATGCCACATGATGATGCAAGCAGTGTGCCAGCTT 1267
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1268 AATGGTGTGAACACGAGATTTCCCAATGATGGTCAATGCTTTCCAACTGGACACAGC 1327
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1328 CAGCCTTGCTCTCTTCGAGTGCTACATGATATACATCACTTCTGGATATGGTCAATGG 1387
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
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481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1448 TCGTACGATGCCAACCGGAGTCCAGTTTACATTTGGGGAGGACCTCCAAACACTGCCCT 1507
501 AsnAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyValLeuVal 520
1508 GATGACGCGCAGCACATGTAGACCTTGTGTGTACCGGACCTCTGTGTGGGTGCTGGTG 1567
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
1568 TGTCAACACCAACACTTCCCGTGGGCGGATGCCACGCTGTGGAGAGGAAATGGTGT 1627
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
1628 ATCAACGGCAAGTGTGTGAACAAACCCACAGAAAGCATTTTGATACGCTTTTTCATGGA 1687
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
1688 AGCTGGGGATGTGGGGGCTTGGGGAGACTGTTCGAGAACCTGCTGGTGGAGAGTCCAG 1747
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
1748 TACACCATGAGGGAATGTACACACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAAGGC 1807
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
1808 AATCAGTGGCTACAGATCTGTACCTTGAGGACTGTCCAGACAAATATGGAAGAAACC 1867
621 PheArgGluGlnCysGlnAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
1868 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTCAAAAGCTTCTTTGGAGTGGG 1927
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
1928 CTGCGGTGGAATGGATCCCAAGTACGCTGGCGTCTCCAAAGACAGAGTGCAGGTC 1987
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
1988 ATCTGCCAAGCAAGGCAATGGCTACTTCTTCGTTTCCAGCCCAAGGTTGTAGATGT 2047

681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
2048 ACTCCATGTAGCCAGATTCACCTCTCTGTGTGCAAGGACAGTGTGTAAAGCTGGT 2107
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2108 TGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAAATGTGTGTTTGGCGGAAAT 2167
721 GlySerThrCysLysLysLysSerValThrSerAlaLysProGlyTyrHisAsp 740
2168 GGATCTACTTGTAAATAAATATCAGGATCAGTTACTAGTCAAAACCTGGATATCATGAT 2227
741 IleIleThrIleProThrGlyValaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
2228 ATCATCAAAATCCAACTGGAGCCACCAACATCGAAGTGAACACAGCGAACAACAGGGGA 2287
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
2288 TCCAGGAACAATGGCAGCTTCTTCCCATCAAGCTGTGATGGCACATATATCTTAAT 2347
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2348 GGTGACTACACTTGTCCACCTTAGAGCAAGACATTAATGTCAAAAGGTTGTCTTAGG 2407
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
2408 TACAGCGCTCTCTCTGGGCAATTCGAAAGAAATTCGACCTTTAGCCCTCTCAAGAGGCC 2467
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
2468 TTGACCATCCAGTCTTACTGTGGGCAATCCCTTCGACCTAAATTAATAATACACCTAC 2527
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
2528 TTCGTAAAGAAAGAAAGAGGAATCTTCAATGCTATATCCCACTTTTTCAGCATGGGTCAAT 2587
861 GluGlnTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
2588 GAAAGATGGGGCGAATGTCTTAAGTCATGTGAATTTGGGTTGGCAGAGAGACTGGTAGAA 2647
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
2648 TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTCCAAAGGAAGTGAAGCCAGCCAGC 2707
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
2708 ACCAGACCTTGTGCAGACCATCCCTGCCCGCAGTGGCAGCTGGGGGAGTGTGTCTCATGT 2767
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
2768 TCTAAGACCTGTGGAGAGGTTACAAAAGAGAGCTTTGAAGTGTCTGTCCCATGATGGA 2827
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
2828 GGGGTGTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGATTT 2887
961 CysThrMetAlaGluCysSer 967
2888 TGCACATGGCAGAAATGCAGT 2908

RESULT 3

US-09-392-184-1
; Sequence 1, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 4858

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(4858)

OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)

NAME/KEY: misc feature

LOCATION: (1)...(4858)

OTHER INFORMATION: n = A,T,C or G

US-09-392-184-1

Alignment Scores:

Pred. NO.: 0 Length: 4858

Score: 5219.00 Matches: 957

Percent Similarity: 99.28% Conservative: 4

Best Local Similarity: 98.86% Mismatches: 6

Query Match: 98.71% Indels: 1

DB: 4 Gaps: 0

US-09-373-658c-126 (1-967) x US-09-392-184-1 (1-4858)

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Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 514 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCGCGTACCCACGCTGCTGCTCGCC 573
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 574 GCGCGCTACTTGGCGGTGTGGAGCGACTCGGGCGCCCTCCGAGGAGGACGAGCTA 633
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 634 GTGTGTCGGAGCTGGAGCGCGCCCGGACACGCGGACCGCGCCCTCCGCTCGACGCC 693
Qy 81 PheAspGlnGlnLeuAspValProProAspSerPheLeuAlaProGlyPhe 100
Db 694 TTTGACAGCAGCTGTGAGTCTGGAGCTGGCGCCCGACAGCAGCTTTTGGCGCCGCTTC 753
Qy 101 ThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGluThrAspLeu 120
Db 754 ACGCTCCAGAACGTGGGGCGCAATCCGGTCCGAGACCGCGCTTCGGGAACCGACCTG 813
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
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Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 874 CTCTCGCGAGGCGTGGCGCGCCCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCG 933
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLeuLysProProAlaPro 180
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Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
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Qy 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
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Qy 281 TyrLeuLeu-ThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAs 300
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Qy 300 nSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGln 320
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Db 1594 TCCAGCAGAGGCTGCTCCGCTATAGAGATGATGTTTACAAAGCTGCTTCCACACAGC 1653
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Db 1654 CCATGAATTAGGCCACCGTGTAAATGCACATGATGATCAAGCAGTGTGCCAGCCT 1713
Qy 420 uAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSe 440
Db 1714 TAAATGTGTGAACCGAGATTCACCATGATGGGCTCATGCTTTCACCTGACCAACAG 1773
Qy 440 rGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGl 460
Db 1774 CCAGCCTTGGTCTCTCTTGGAGTGCCTACATGATTAATCATATTTCTGGATAATGGTCA 1833
Qy 460 yGluCysLeuMetAspIleProGlnAsnProIleGlnLeuProGlyAspLeuProGlyTh 480
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Qy 480 rSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPr 500
Db 1894 CTGTAAGATGCCAACCGGCGAGTCCAGTTTACATTTGGGAGGACTCCCAACACTGCCCC 1953
Qy 500 oAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVa 520
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Qy 520 lCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCy 540
Db 2014 GTGTCAAAACCAACATTTCCGTTGGCGGATGGCACCAGCTGTGGAGAGGAAATGGTG 2073
Qy 540 sIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGl 560
Db 2074 TATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTCATGG 2133
Qy 560 ySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 2134 AAGCTGGGAATGTGGGGGCTTGGGGAGACTGTTGAGAACCGTGGCTGGAGAGTCCA 2193
Qy 580 nTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysIleLysTyrCysGluGl 600
Db 2194 GTACACGATGAGGAGATGTGACACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGG 2253
Qy 600 yLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysTh 620
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Db 2254 CAAACGAGTGGCTACAGATCTGTAACTTGGAGACTGTCCAGACAATAATGGAAAAAC 2313
Qy rPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGI 640
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Qy 640 yProAlaValGluTrrPileProLysTyrAlaGlyValSerProLysAspArgCysLysLe 660
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Qy 660 uileCysGlnAlaLysGlyLeuGlyPhePheValLeuGlnProLysValValAspGI 680
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Db 2554 TTGTGATCGCATCATAGACTCCAAAAGAAAGTTTGATAATGTGGTGTTCGGGGGAAA 2613
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Qy 760 ySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAs 780
Db 2734 ATCCAGGACAAATGGCAGCTTCTTCCCATCAAGCTGTGTGGCACATATATCTTAA 2793
Qy 780 nGlyAspTyrThrLeuSerThrIleuGlnAspIleMetTyrLysGlyValValLeuAr 800
Db 2794 TGGTGACTACACTTGTCCACCTTAGCAAGACAGCATATATCAAAAGTGTGTCTTAG 2853
Qy 800 gTyrSerGlySerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPr 820
Db 2854 GTACAGCGGCTCTCTCGCGCATGGAAAGAAATTCGACGTTTAGCCCTCTCAAGAGCC 2913
Qy 820 oLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTy 840
Db 2914 CTTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACCTTAAATTAATACACCTA 2973
Qy 840 rPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrrValI 860
Db 2974 CTTGTAAGAGAGAGAGAGAAATCTTCAATGCTATCCCACTTTTTCAGCATGGGTCA 3033
Qy 860 eGluGluTrrPlyGluCysSerLysSerCysGluLeuGlyTrrPdnArgArgLeuValGI 880
Db 3034 TGAAGAGTGGGGCAATGTTCTAAGTCATGTGAATTTGGGTGGCAGAGAACTGGTAGA 3093
Qy 880 uCysArgAspIleAsnGlyGlnProLysArgCysAlaLysGluValLysProAlaSe 900
Db 3094 ATGCCAGACATTAATAGCAGCTCTTCCGAGTGTGCAAGAGAGTGAAGCCAGCCAG 3153
Qy 900 rThrArgProCysAlaAspHisProCysProGlnTrrPdnLeuGlyGluTrrPdnSerSerCy 920
Db 3154 CACCAGACCTTGTGCAGACCATCCCTGCCAGTGGGAGCTGGGGAGTGTGCATCATG 3213
Qy 920 sSerLysThrCysGlyLysGlyTrrLysLysThrSerLeuLysCysLeuSerHisAspGI 940
Db 3214 TTCTAGACCTGTGGGAAGGGTTACAAAAAGAGAGCTTGAAGTGTCTGTCCCATGATGG 3273
Qy 940 yGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPh 960
Db 3274 AGGGGTGTTATCTCATGAGAGCTGTGATCTCTTAAAGAAACCTTAACATTTTCATAGACT 3333
Qy 960 eCysThrMetAlaGluCysSer 967
Db 3334 TTGCACATGGCAGATGTCAGT 3355

RESULT 4

US-09-484-970B-58
: Sequence 58, Application US/09484970B
: Patent No. 6426186
: GENERAL INFORMATION:
: APPLICANT: Jones, Karen A.
: APPLICANT: Volkmer, Wayne
: APPLICANT: Walker, Michael G.
: TITLE OF INVENTION: BONE REMODELING GENES
: FILE REFERENCE: PB-0014 US
: CURRENT APPLICATION NUMBER: US/09/484,970B
: CURRENT FILING DATE: 2000-01-18
: NUMBER OF SEQ ID NOS: 172
: SOFTWARE: PERL Program
: SEQ ID NO 58
: LENGTH: 3706
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No. 6426186 007074.1
: LOCATION: 3634, 3638-3639, 3642-3643, 3647-3648, 3652, 3654-3658, 3674, 3681
: OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-58

Alignment Scores:

Pred. No.: 0 Length: 3706
Score: 4262.00 Matches: 772
Percent Similarity: 99.36% Conservative: 1
Best Local Similarity: 99.23% Mismatches: 4
Query Match: 80.61% Indels: 1
DB: 4 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-484-970B-58 (1-3706)

Qy 191 GlnGlyAspValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLys 210
Db 3 CAGGGCGAGCTAGGCGGCACCTGCGGGGTCTGGACGACGAGCCCGCCGACCTGGAAA 62
Qy 211 AlaGluThrGluAspGluAspGluGlyThrGluGluAspGluGlyProGlnTrrSer 230
Db 63 GCGGAGACCGAAGACGAGGACGAGGAGCTGAGGGCGGAGGACGAGGGCCCTCAGTGGTGG 122
Qy 231 ProGlnAspProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLys 250
Db 123 CCGCAGGACCGCGGCACTGCAAGGGGTAGGACAGCCACAGGAACTGGAAGCATAGAAG 182
Qy 251 LysArgPheValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMet 270
Db 183 AAGCGATTGTGTCCAGTCACCGCTATGTGGAACCATGCTTGTGGCAGACCCAGTCCGATG 242
Qy 271 AlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAla 290
Db 243 GCAGATTCCAGGCGAGTGTCTAAGCATTTACCTTCTTCAGTTGTTTTCGGTGGCAGCC 302
Qy 291 ArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValValLysIleLeu 310
Db 303 AGATTGTACAAACACCCCGACCATTCGTAATTCAGTTAGCTGTGTGGTGGTGAAGATCTTG 362
Qy 311 ValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArg 330
Db 363 GTCATCCAGATGAACAGAGAGGGCGGAGTACCTTCAATGCTGCCCTCCTCCTCTGGG 422
Qy 331 AsnPheCysAsnTrrPdnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyr 350
Db 423 AACTTTGCACCTGGCAGACGACGACACACCCAGTACCAGGATGCGAGACCTAT 482
Qy 351 AspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeu 370
Db 483 GACACAGCAATTTCTTTTCCACAGACAGGACTTGTGTGGTGGTGGTGGTGGTGGTGGTGGT 542

371 GlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValIleGluAsp 390
543 GGGATGGCTGATGTTGGAACTGTGTGATCCGAGCAGAAAGCTGCTCCGCTCATAGAAGAT 602
391 AspGlyLeuGlnAlaAlaPheThrThrAlaHisGluGlyHisValPheAsnMetPro 410
603 GATGGTTTACAGCTGCCCTTCCACACAGCCCATGAATTAGGCCACCTGTTTACATGCCA 562
411 HisAspAlaAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMet 430
663 CATGATGATGCAAGAGAGTGTGCCAGCCTTAATGTTGTGAACCCAGGATCCACATGATG 722
431 AlaSerMetLeuSerAsnLeuAspHisSerGlnProThrSerProCysSerGlyTyrMet 450
723 GCGTCATGCTTCCAACTGGACACAGCCCTGGGTCTCCCTTGCAGTGGCTTACATG 782
451 IleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnPro 470
783 ATTACATCATCTCGATATGTCATGCGGAATGTTTGTATGGACCAAGCTCAGATATCCC 842
471 IleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490
843 ATACAGCTCCACAGCGCATCTCCCTGGCACCCTCTACGATGCCAACCGGAGTCCAGTTT 902
491 ThrPheGlyGlnAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTyr 510
903 ACATTTGGGAGAGACTCCAAACACTGCCCGATGCAGCCAGCACATGTAGCACCTTTGG 962
511 CysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProThrAlaAsp 530
963 TGTACCGGCACCTCTGTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1022
531 GlyThrSerCysGlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysAsnHis 550
1023 GGACACAGCTGTGGAGAAGGAAATGTTGATCAACGGCAAGTGTGTGTGTGTGTGTGTGTGT 1082
551 ArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProThrGlyAsp 570
1083 AGAAGCAATTTGATACGCTTTTTCATGGAAGCTGGGGATGTTGGGGGCTTGGGAGAC 1142
571 CysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProVal 590
1143 TGTTCGAGAACGTGCGGTGGAGGAGTCCAGTACAGATGAGGGAATGTGCAACCCAGTC 1202
591 ProLysAsnGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeu 610
1203 CCAAGGAATGGAGGAAGTACTGTGAAGGCAACAGAGTGGCTACAGATCTGTACCTT 1262
611 GluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsn 630
1263 GAGGACTGTCCAGACAATATGGAAAAACCTTTAGAGAGGAACAATGTGAAGCACAACAC 1322
631 GluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrPheProLysTyrAla 650
1323 GAGTTTTCAAAAGCTTCTCTTGGGAGTGGGCTCGGTGGATGGATTCGAGTAGCCT 1382
651 GlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhe 670
1383 GCGCTCTCCACAAAGGACAGGTGCAAGCTCATCTGCCAAGCAAGCAATGGCTACTTC 1442
671 PheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerVal 690
1443 TTCCTTTTGCAGCCCAAGGTTGTAGATGGTACTCCATGTAGCCAGATTCACCTCTGTC 1502
691 CysValGlnGlnGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLys 710
1503 TGTGTGCAGAGCAGTGTGTAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1562
711 PheAspLysCysGlyValCysGlyAsnGlySerThrCysLysLysIleSerGlySer 730
1563 TTTGATAAATGTGTGTGTGGGGGAAATGATCTACTTGTAAATAAATATATCAGATCA 1622
731 ValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsn 750

1623 GTTACTAGTGCAAAACCTGGGATATCATGATATCATCAATTCCAATTCGAGCCACCAAC 1682
751 IleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsn-GlySerPheLeuAlaIle 770
1683 ATCGAAGTGAAACAGAGCGGATCCAGAGGGGATCCAGGAAACAATGGGCAGCTTTCTTGCCAT 1742
770 elysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGln 790
1743 CAAGCTGCTGATGGCACATATTTCTTAATGGTGACTACACTTTGTTCACCTTAGAGCA 1802
790 nAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArg 810
1803 AGACATTATGTACAAAGTGTGTCTTCAGGTACAGCGGCTCTCTCGGGCATTTGGAAAG 1862
810 gIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAs 830
1863 AATTCGACGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTCTTACTTGTGGGCAA 1922
830 nAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPheAs 850
1923 TGCCCTTCGACCTAAATTAATACACTACTTCTGTAAAGAGAAGAAGAAATCTTTCAA 1982
850 nAlaIleProThrPheSerAlaIleValIleGluTyrGlyGluCysSerLysSerCys 870
1983 TGCTATCCCACTTTTTCAGCATGGGTCAATTGAAGAGTGGGGCGAATGTTCTAAGTCATG 2042
870 sGluLeuGlyTyrGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSe 890
2043 TGAATGGGTGGCAGAGAGACTGTGTAGAAATGCCGAGACATTAATGGACAGCTGCTTC 2102
890 rGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCysPr 910
2103 CGAGTGTGCAAGGAAGTGAAGCCAGCCAGCAGCAGACCTTGTGCAGAGCATCCCTGCC 2162
910 cGlnTrpGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGlyTyrLysLys 930
2163 CCAGTGGCAGCTGGGGAGTGTGTATGTTCTAAGACCTGTGGGAAGGTTTACAAAA 2222
930 sThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSerCysAspPr 950
2223 AAGAGCTTGAAGTGTCTGTCCCATGATGGAGGGTGTATCTCATGAGAGCTGTGATCC 2282
950 oLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
2283 TTTAAAGAAACCTAAACATTTTCATAGACTTTTGCAACAATGGCAGAAATGCAGT 2334

RESULT 5

US-09-445-023A-2

Sequence 2, Application US/09445023A

Patent No. 6565858

GENERAL INFORMATION:

APPLICANT: Hirose, Kunitaka

APPLICANT: Inoguchi, Eiichi

APPLICANT: Hakozaeki, Michinori

APPLICANT: Ishioaka, Keiko

APPLICANT: Ishida, Yukako

APPLICANT: Matsushima, Kouji

APPLICANT: Kuno, Kouji

TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical

composition and method of immunologically analyzing human ADAMTS.

FILE REFERENCE: 057092

CURRENT APPLICATION NUMBER: US/09/445,023A

CURRENT FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: JP 9-160422

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 2184

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

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; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-2

Alignment Scores:
  Pld. No.:      0      Length:      2184
  Score:      3922.00    Matches:      707
  Percent Similarity: 98.89%    Conservative: 5
  Best Local Similarity: 98.19%    Mismatches: 8
  Query Match:      74.18%    Indels:      0
  DB:      4      Gaps:      0

US-09-373-658c-126 (1-967) x US-09-445-023A-2 (1-2184)

QY 248 lIeArgLysLysArgPheValSerHisArgTyrValGluThrMetLeuValAlaAsp 267
DB 22 CTTAGAAAGACGAGTTTGTGTCAGCCGCCCTTATGTGGAACCATGCTTGTGCGAC 81
QY 268 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 287
DB 82 CAGTCGATGGCAGAAATCCACGCGCAGTGGTCTAAGACATTACCTTCTCAAGTTGTTTCG 141
QY 288 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 307
DB 142 GTGGCAGCGAGATTGTACAAACACCCAGCATTCGTAAATTCAGTTAGCTGTGTGTGTG 201
QY 308 LysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeu 327
DB 202 AAGATCTTGTCATCCACGATCAACAGAGGGGCGGAGTGACCTCCCAATGCTGCCCTC 261
QY 328 ThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAla 347
DB 262 ACTCTGCGGAATTTTGCACATGGCAGAGCAGCAGCAACCCACCGAGTGACCGGATGCA 321
QY 348 GluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCys 367
DB 322 GAGCATATGACACAGCAATTTCTTTCCACAGCAGGACTTGTGTGGTCCACAGCATGT 381
QY 368 AspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerVal 387
DB 382 GATACTCTTGGGATGGCTGATGTGCACTGTGTGTGATCCGAGCAGAGCTGCTCCGTC 441
QY 388 lIeGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhe 407
DB 442 ATAGAGATGATGGTTTACAGCTGCTTCCACAGCCCATGAATTAGGCCACCGTGTTT 501
QY 408 AsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSer 427
DB 502 AACATGCCACATGATGATCAAGCAGTGTGCCAGCTTAAATGGTGTGAACCCAGGATTCC 561
QY 428 HisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSer 447
DB 562 CACATGATGGCTCAATGCTTTCCAACTGGGACCAACGCCAGCCCTTGTCTCTTTCAGT 621
QY 448 GlyTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysPro 467
DB 622 GCCTACATGATTACATCACTTCTGATATATGTCATATGGGAATGTTTGTATGACCAAGCT 681
QY 468 GlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGln 487
DB 682 CAGAAATCCCATACAGCTCCAGCGCATCTCCCTGGCACCCTTGTAGCATGCCAACCGGAG 741
QY 488 CysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 507
DB 742 TCCAGTTTACATTTTGGGGAGGACTCCAAACACTGCCCGCATGCCAGCAGCATATGTAGC 801
QY 508 ThrLeuTrpCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPhePro 527
DB 802 ACCTTGTGGTGTACCGCACCTCTGTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
QY 528 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 547
DB 862 TGGCGGATGGCACCAGCTGTGGAGAGGAAATGGTGTATCAACGGCAAGTGTGTGAAC 921
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QY 548 LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 567
DB 922 AAAACCCAGCAGGAAGCATTTTGATACGCCCTTTTATGGAAGCTGGGACCAATGGGAGCCG 981
QY 568 TrpGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAsp 587
DB 982 TGGGAGACTGTTTCAGAACCGTGGTGGAGGAGTCCAGTACAGATGAGGAGAAATGTGAC 1041
QY 588 AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer 607
DB 1042 AACCCAGTCCCAAGAATGGAGGGAAGTACTGTGAAGGCAACAGTGCCTAGCATGCC 1101
QY 608 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlyCysGlu 627
DB 1102 TGTAACTTGGAGACTGTCCAGACAATAATGGAARAAACCTTTAGAGGAGAAATGTGAA 1161
QY 628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIlePro 647
DB 1162 GCACACACAGAGTTTCAAAAGCTTCTTTGGGAGTGGGCTGCGGTGGAAATGGAATCCC 1221
QY 648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle 667
DB 1222 AAGTACGCTGGGCTCTCACCAAGSACAGGTGCAGGTCTCATCTGCCAAGCCAAAGGCATT 1281
QY 668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
DB 1282 GGCTACTTCTTGTTTGCAGCCCAAGGTGTTGATGCTGATCTCCATGTAGCCAGATTCC 1341
QY 688 ThrSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSer 707
DB 1342 ACCTCTGTGTGTGCAAGGACAGTGTGTAAAGCTGGTGTGTGATCGCATCATAGACTCC 1401
QY 708 LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle 727
DB 1402 AAAAAGAGTTTGATAAATGTTGTTTGGGGGAAATGGATCTACTTGTAAAAAATA 1461
QY 728 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 747
DB 1462 TCAGGATCAGTACTAGTGCACAAACCTGGATATCATATATCGTCAAAATTCACACTTGA 1521
QY 748 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 767
DB 1522 GCCACCAACATCGAAGTGMAACAGCGGACCCAGAGGGGATCCAGAACCAATGGCAGCTTT 1581
QY 768 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 787
DB 1582 CTTGCCATCAAGCTGCTGATGGCACATATATCTTAATGGTGTACTACACTTGTGTCCACC 1641
QY 788 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 807
DB 1642 TTAGGCAAGCATATGTACAAAGGTGTGTCTTGAGGTACAGCGGCTCTCTCTGCGCA 1701
QY 808 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 827
DB 1702 TTGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGGCCCTTGACCATCCAGGTTCTTACT 1761
QY 828 ValGlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysGlu 847
DB 1762 GTGGCAATGCCCCCTTCGACCTTAAATTAATACACCTACTTCTGTAAGAGAGAGAGAA 1821
QY 848 SerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSer 867
DB 1822 TCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCTATGGAAGAGTGGGCGCAATGTCT 1881
QY 868 LysSerCysGluLeuGlyTyrGlnArgLeuValGluCysArgAspIleAsnGlyGln 887
DB 1882 AAGTCATGTGAATGGGTGGCAGAGAGACTGTGTAGAAATGCCAGACATTTAATGGACAG 1941
QY 888 ProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHis 907
DB 1942 CCTCTTCCGAGTGTGCACAAAGGAAGTGAAGCCAGCCAGCAGACCTTGTGCAGACCAT 2001
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Qy 908 ProCysProGlnTyrGlnLeuGlyGluTyrSerSerCysSerLysThrCysGlyLysGly 927
Db 2002 CCGTGGCCCCAGTGGCAGCTGGGGAGTGGTCAATCATGTTCTAAGACCTGTGGAGGGT 2061
Qy 928 TyrLysLysThrSerLeuLysCysLeuSerHisAspGlyGlyValLeuSerHisAspSer 947
Db 2062 TACAAAAAGACAGCTTGAAGTGTCTGCCATGATGGAGGGGTATTCTCATGAGAGC 2121
Qy 948 CysAspProLeuLysLysProLysHisPheLeuAspPheCysThrMetAlaGluCysSer 967
Db 2122 TGTGATCCITTTAAAGAAACCTAAACATTTTCATAGACTTTTGCACACTGCACACAGTGCAGT 2181
RESULT 6
US-09-445-023A-13
; Sequence 13, Application US/09445023A
; Patent No. 6563858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioaka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; TITLE OF INVENTION: composition and method of immunologically analyzing human ADAMTS
; FILE REFERENCE: 057092
; CURRENT APPLICATION NUMBER: US/09/445,023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)..(2184)
US-09-445-023A-13

Alignment Scores:
Pred. No.: 0 Length: 2184
Score: 3652.00 Matches: 646
Percent Similarity: 94.77% Conservative: 43
Best Local Similarity: 88.86% Mismatches: 38
Query Match: 69.08% Indels: 0
DB: 4 Gaps: 0
US-09-373-658C-126 (1-967) x US-09-445-023A-13 (1-2184)

Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1 AAGCCATCAGGACCCAGGACCATTAAGGAGAGCGGATTGTGTCCAGCCCCCGTTATGTG 60
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 61 GAAACCATGCTGCTAGTGCACCGAGTCCATGCCGAGCTTCCACGCGACGCGTCTAAAGCAT 120
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 121 TACCTTCAACCCCTGTTCTCGTGGCAGCAGCGTTTACAAAGCATCCAGCATTAGGAAT 180
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 181 TCAATTAGCCCTGGTGGTGGTGGAGATCTTGCTCATATATACGAGGAGCAGAGGACAGAA 240
Qy 321 ValThrSerAsnAlaAlaThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
Db 241 GTACCTCCCAATGAGCTCTCACCCCTTCGGAAATTTTCGAGCTGGCAGAAACCAAC 300
Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360

Db 301 AGCCCCAGTGACCGGGATCCAGAGCACTATGACACTGCAATTCGTTCACCACACAGGAT 360
Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 361 TTATGTGGCTCCACACACGCTGTGACACTCTCGGAATGGCAGATCTTGGAAACCGTATGTGAC 420
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 421 CCAGCAGAGAGCTGCTCATGATAGAGATGATGTTTGAAGCTGCTTCACAGCTCCCTTCACACAGCC 480
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 481 CATGAATGGCCCATGTGTTAAACATGCCCGCAGATGATGTAAGCAGCTGTGCCAGCTTG 540
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 541 AATGGTGTGATGGCGGATCTCATGATGGCTCGATGCTCTCCAGCTTAGACCATAGC 600
Qy 441 GlnProTyrSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 601 CAGCCCTGGTCACTTGGCAGTGCCTACATGGTCACTGCTCTCTAGATATATGACACAGCG 660
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 661 GAATGTTTTCATGGACCAAGCCCGAGATCCCAATCAAGCTCCCTTCTGATCTTCCCGGTACC 720
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 721 TTGTAGCATGCCAACCCGAGTGTGAGTTTACATTCGGAGAGAAATCCAAAGCACTGCCCT 780
Qy 501 AspAlaAspThrCysSerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuVal 520
Db 781 GATGAGCCAGCACATGTACTACCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 521 CysGlnThrLysHisPheProTyrAlaAspGlyThrSerCysGlyGluGlyLysTyrCys 540
Db 841 TGCCAAACAAACACATTCCTTGGGAGATGGCAGCTGTGGAGAGGAGGAGTGGTGT 900
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 901 GTCAGTGGCAAGTGGTGAACAGACAGACATGAAGCATTTGCTACTCTCTGTTCAATGA 960
Qy 561 SerTyrGlyMetTyrGlyProTyrGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
Db 961 AGCTGGGGCCATGGGGACCGTGGGAGACTGCTCAAGAACCTGTGCTGCTGCTGCTGCTGCT 1020
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 1021 TACCAATGAGAGATGTGACAAACCCGCTCCCAAGAACCGAGGAGAGTACTGTGAGGC 1080
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
Db 1081 AAACAGTCCGCTACAGGTCCTGTAAACATCGAGGACTGTCCAGACAAATTAACGAAACAG 1140
Qy 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 1141 TTCAGAGAGAGAGTGGCAGGCGGACATGATGTTTTCAAAGCTTCCTTTTGGAAAGAG 1200
Qy 641 ProAlaValGluTyrIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 1201 CCCACTGTAGTGGACACCCCAAGTACGCGCGCTGCTGCCAAAGGACAGGTCAGAGCTC 1260
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValAlaAspGly 680
Db 1261 ACCTGTGAAGCCAAAGGCAATGGCTACTTTTTCGCTTACAGCCCCAAGGTGTGAGATGGC 1320
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 1321 ACTCCCTGTAGTCCAGACTCTACTCTCTGTGTGCAAGGCGAGTGTGTGAAGCTGCG 1380
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720

255 SerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHis 274
256 TCGAGCGCTCGCTTCTGGTGGAAACACTTCTGTGGCTGATCGTCCATGGCTGCTTCTAT 1027
275 GlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLys 294
1028 GGGACCGACCTGCAGAACCACTCTCACTGATGTCAATGGCAGCCCGCAATCTACAAG 1087
295 HisProSerIleArgHisSerValSerLeuValValValLysIleLeuValIleHisAsp 314
1088 CACCCGAGCATCAGGAACCTCCGTAACCTTGTGGTGGTGAAGTGTAAATAGTGGAAAA 1147
315 GluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgHisPheCysAsn 334
1148 GAAAGATGGGGCCCGGAGTGTCCGACACGGGGGGCTCACACTGGCGCACTTCTGCAGC 1207
335 TrpGlnLysGlnHisIleAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIle 354
1208 TGGCAACGGGGTTTCAACAGCCCGAGTGCACCGCAGCCCGGAGCACTATGACATGCCATC 1267
355 LeuPheThrArgGlnAspLeuCysGly---SerGlnThrCysAspThrLeuGlyMetAla 373
1268 TTGTTCACACAGACAGACTTCTGTGGAGAGGGAGAGCAGTGTGACACCTTGGGGATGGCA 1327
374 AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspGlyLeu 393
1328 GACGTTGGCACCATCTGTGACCCCGACAGAGCTGTCTAGTATCAAGGATGAGGACTG 1387
394 GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp 413
1388 CAGGACGCTTACACCTCGGCCCATGAGTAGGSCAGCTTCTCAGCATGGCCCCATGATGAT 1447
414 AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMet 433
1448 TCTAAGCCCTGTGTGAGATTGTTGGGCCCATGGGCAAGTACCATGATGGCGCCATTC 1507
434 LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer 453
1508 TTCATCCAGCTGAACAGAGCTGCTGTCTCTCCCTGCAGCTGTCTACTACCTCACAGAG 1567
454 PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu 473
1568 CTCCTGGATGATGTCACGAGATGTTCTTCTGGATGCCGCCACCTCGGTTCTGCCCTTC 1627
474 ProGlyAspLeuProGly-----ThrSerTyrAspAlaAsnArgGlnCysGlnPheThr 491
1628 CCCACAGGCTCCCGGCCACAGACCTCTACGAGCTGGACAGCAGCAGTGCACAGCAGATC 1687
492 PheGlyGluAspSerLysHisCysProAspAlaAla-----SerThrCysSerThrLeu 509
1688 TTTGGGCTGATTTCCAGACACTCCCACTCCCACTCTGTGGAGGACATCTGTGTCCAGCTC 1747
510 TrpCysThrGlyThrSerGlyValLeuValCysGlnThrLysHis-----PhePro 527
1748 TGTGCCCGTTCATCGGATAGTATGAGCCCATTTGCCACAAAGAAATGATGATGCTGCTC 1807
528 TrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsn 547
1808 TGGGCTGATGGTACACCTGTGSCCTCGGCCACTGTGCTGCTGATGGTGGTGTGATCTC 1867
548 LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro 567
1868 AAGAGGATGTGGAGATCCAGAGCTGTGTGATGGAGACTGGGGTCCCTGGAGACCC 1927
568 TrpGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAsp 587
1928 TGGGGACATCTTCTCCACCTGTGTGGTGGAGGATACATTTCTCGAACCCGTGAATGTGAT 1987
588 AsnProValProLysAsnGlyLysValTyrCysGluGlyLysValArgValArgTyrArgSer 607
1988 AATCCATGCTCAGAAATGGAGAGATTTTGTCTGGTGGTGAAGAGTCAAGTACCAATCA 2047
608 CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCysGlu 627

2048 TGCACACAGAGAAATGCCACCA---AACGGAAGAAGCTTCGGAGGAGCAGAGTGTGAG 2104
628 AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIlePro 647
2105 AAATATAATAGCTTACAAACCACTACACTGACCTG---GATGGGAATTTCTGTGAGTGGTCCCC 2161
648 LysTyrAlaGlyValSerProLysAspArgCysLysLeuLeuLeuCysGlnAlaLysGlyIle 667
2162 AAGTATTTCAGGAGTGTCCCCCGAGCAGCAGTCAAGCTGTTTTCAGAGACCCGCGGGAGG 2221
668 GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer 687
2222 AGTGAGTTCAAAGTGTGTAAGCTAAGGTGATGCACTCTGTGTGGACGGGATACT 2281
688 ThrSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSer 707
2282 CTGTTCATCTGCTCGGGGGCAATGTGTTAAGCTGGCTGACCATGTGTGTGAATCA 2341
708 LysLysLysPheAspLysCysGlyValCysGlyValGlyAsnGlySerThrCysLysLysIle 727
2342 CCTAAGAGCTGCACAAATGTGGGGTGTGGGGCAAGGCACTGCCTGTAGGAAGATC 2401
728 SerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThrGly 747
2402 TCCGGTCTCTTTCACCCCTTCACTTATGCTTATGCTACAATGACATTTGTACCACATCCAGCTGT 2461
748 AlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPhe 767
2462 GCACAAACATTTGATGTGAAACAGCGGAGTCAACCCAGGGCTCAGGACACGCGCAGCTAC 2521
768 LeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThr 787
2522 CTGGCGCTGAAACAGACCAATGGGAGTACCTGTCTCAATGGTAAACCTGTGCCATCTCTGCC 2581
788 LeuGluGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAla 807
2582 ATAGAGCAGACATCTTGTGAGGGGACCATCTCTGAGTACAGTGGCTTCCATGGCTACC 2641
808 LeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThr 827
2642 CTGGAGCGCTGCAGAGCTTCCAGGCCCTGCGCTGAGCGCTTCTTACAGTACAGCTCTCTGACT 2701
828 Val---GlyAsnAlaLeuArgProLysIleLysTyrThrTyrPheVal----- 842
2702 GTGTGTGGTGGTCTTCCCTCCAAAGTCAAGTATATCTTCTTGTGCCCAATGACATG 2761
843 -----LysLysLysLysGluSerPheAsnAlaIleProThrPhe--- 855
2762 GACTTCAGCGCTGCAGATAGCAAGGAGAGCAGCACCAACATCATTCAGTCACTGCC 2821
856 ---SerAlaTrpValIleGluLutrpGlyGluCysSerLysSerCysGluLeuGlyTrp 874
2822 TCTGGGAGTGGGTTCTGGGAGACTGGTCTGAATGCCAGCAGCAGCTGAGAGTGTGG 2881
875 GlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLys 894
2882 CAGCGCGGAGCTGTGGATGCGAGGACCCCTCAGTCAAGCTCAGGACCTGTGATGAG 2941
895 GluValLysProAlaSerThrArgProCysAlaAspHisProCysPro-----Gln 911
2942 GCTCTGAAACCTGAGGATGCCAAGCCCTGTGGAAGCAGCCCGTGTCCCTCTGATCCCT 3001
912 Trp-----GlnLeuGlyGluTrpSerSerCysSerLys 922
3002 TGGTGGAAATCTCTTAGGCTTATGAGTTGGGCTACTGG-----TGTAAACAGA 3049

RESULT 8
US-09-392-184-7/c
; Sequence 7, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION
; APPLICANT: Robison, Keith E.

D	B		2535	TGTGGCAGCCCGCAATCTACAGCACCCCAGCATCAAGAATTCCATCAACCTGATGTTGGT	2476
Q	Y		307	lysllelleuValIleHieAspGluInLysGlyProGluValThrSerAsnAlaIale	327
D	B		2475	AAAAGTGCTGATCGTAGAAGATGAATAATTTGGGGCCCCAGAGGTGTTCGCACAATGGGGGCT	2416
Q	Y		327	uThrLeuArgAnPheCyAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAl	347
D	B		2415	TACACTGGGTAACTTCTGCAACTGSCAGCGGGCTTCAACAGGCCCGAGCCGCCACCC	2356
Q	Y		347	aGluHisTyrrAspThrAlaIleLeuPheThrArgGlnAspLeuCyeGlySerCln---	366
D	B		2355	AGAGCACTACGACACCGCCCATCTCTCTACCACAGACAATCTTGTGGCAGAGGGGCT	2296
Q	Y		366	rCyAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSe	386
D	B		2295	GTTGTACACCCCTGGGTGTGGCAGACATCGGACCATTTGTGACCCCAAACAAAGCTGCTC	2236
Q	Y		386	rValIleGluAspAspGlyLeuGlnAlaIalaPheThrAlaHisGluLeuGlyHisVa	406
D	B		2235	CGTGATCGAGGATGAGCGCTCCAGCGGCCCCACACCTCTGGGCCCATTAAGTACGAGCAGCT	2176
Q	Y		406	IpheAsnMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAs	426
D	B		2175	CCTCAGCATGCCCCAGACGACTCCAAGCCCTGCACACCGCTCTTCGGGCCCATGGCAA	2116
Q	Y		426	pSerHisMetMetalSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCy	446
D	B		2115	GCACCACTGATGGCACCGCTGTGTCTCCACCTGAACACAGACGCTCCCTGTGTCCTGCTG	2056
Q	Y		446	sSerGlyTyrrMetIleThrSerPheLeuAspAndGlyHis-----G1	460
D	B		2055	CACGCGCATGTATCTCACAGAGCTTCTGACGGGGGGCACCGAATTCAGGTATTTATGCC	1996
Q	Y		460	yGluCysLeu-MetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyT	480
D	B		1995	CCTGTGCTAGTGT-----1982	
Q	Y		480	hrSerTyrrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysP	500
D	B		1981	-----CTACAGCGTGCATTATGCTCTTTGGCGCGAATTCGSCACATGCC	1936
Q	Y		500	roAsp-----AlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyV	518
D	B		1935	CCACACTCTGCTCAGGACGCTCGGCCAGCTTTGGTGC---CACACTGATGGGGCTG	1879
Q	Y		518	alLeuValCysGlnThrLysHis-----PheProTrpAlaAspGlyThrSerCysGlyG	536
D	B		1878	AGCCCTGTGCCACAGAAATGGCAGCGCTGCTCTGGCTGCAGCGCAGCCGCTGGGGGC	1819
Q	Y		536	luGlyLysTrpCylleAsnGlyLys-CysValAsnLysasnHisargLysHisPheAsp	555
D	B		1818	CTGGCACCTCTCTCAGAAAGGCAAGTGTCTACCTTGAGAGGAAGATGGAGGCCCAAG	1759
Q	Y		556	Thr-ProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCys	575
D	B		1758	CCCGTGTAGATGGAGCTGGGCACCGTGGGACCTCTGGGAGAAATGTTCTCGGACCTGT	1699
Q	Y		576	GlyGlyGlyValGlnTyrrMetArgGluCysAspAsnProValProLysAsnGlyGly	595
D	B		1698	GGAGGAGGAGTACAGTTTTTACACCGCTGATGCAAGGACCCCGAGCTCTCAGAATGGAGGA	1639
Q	Y		596	LysTyrrCysGluGlyLysArgValArgTyrrArgSerCysAsnLeuGluAspCysProAsp	615
D	B		1638	AGATACTGCTCTGGGTGGAGAGCCAGTACAGTCACTGATCCACAGGAGGAATGCCCCCT	1579
Q	Y		616	AsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAla	635
D	B		1578	--GACGGGAAAAAGCTTCAGGGGAGCAGCTGTGAGAAGTATATGCTCTACAATTCACCT	1522
Q	Y		636	SerPheGlySerGlyProAlaValGluTrpIleProLysTyrrAlaGlyValSerProLys	655
D	B		1521	GACATG---GACGGGAATCTCTCGATGGGTCCCCAAGTATGCTGGGGTGTCCCCCGG	1465

Db 958 -----AGTCCTGCCAGCGGTCAAGTCCCATGTCACACGTCGAAGCTCT--- 1002
Qy 236 LeuGlnGlyValGlyGlnProThrGlyThrGlySerIleAglGlyValSer 255
Db 1003 -----CTTGGAGGCCAGCCAGCCAGCCCA---AGAGCCAGCGCTTTCCTTCA 1050
Qy 256 SerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGly 275
Db 1051 CTGAGTAGATTGTGGAGACACTGTGTGGTGGCAGATGACAAAGATGGCCGATTCACGGT 1110
Qy 276 SerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHis 295
Db 1111 GCGGGGCTTAAGCGCTACTGCTAACAGTGTGGCAGCAGCAGCCAGCCCTTCAGGAC 1170
Qy 286 ProSerIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGlu 315
Db 1171 CCNAGCATCCGCAATCTCTGACGTTGTGGTGTGACTCGCTAGTGTGATCTCGGGTTCAGGC 1230
Qy 316 GlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTyr 335
Db 1231 GAGGAGGGGCCCAAGTGGGGCCAGTGTCTGCCAGACCCCTGGCAGCTTCTGTGCCTGG 1290
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Db 1351 TTTACCGGTCAGGACTGTGTGGAGTCTCCACTTCGACACCGCTGGGTATGCTGATGTG 1410
Qy 376 GlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAla 395
Db 1411 GGCACCGTCTGTGACCCGCTCGGAGCTGTGCCATTGTGGAGATGATGGGCTCCAGTCA 1470
Qy 396 AlaPheThrAlaHisGlnLeuGlyHisValPheAsnMetProHisAspAspAlaLys 415
Db 1471 GCTTCTCACTGCTGCTCATGACTGGGTCTATGCTTCTCAACATGCTCCATGACAACTCCCAAG 1530
Qy 416 GlnCysAlaSerLeuAsnGly---ValAsnGlnAspSerHisMetMetAlaSerMetLeu 434
Db 1531 CCATGATCAGTTTGAATGGGCTTTTGACACCTCTCGCCATGTCTATGGCCCTGTGATG 1590
Qy 435 SerAsnLeuAspHisSerGlnProThrProThrSerProCysSerGlyTyrMetIleThrSerPhe 454
Db 1591 GCTCATGTGGATCTCTGAGGAGCCCTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1650
Qy 455 LeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuPro 474
Db 1651 CTGGCAATGGCTATGGGCACTGTCTCTTGAACAAACCAAGAGGCTCCATGTGATCTGCT 1710
Qy 475 GlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGlu 494
Db 1711 GTGACTTTCTCTGGCAAGGACTATGATGCTGACCGCCAGTGCAGTGCACCTTCGGGCC 1770
Qy 495 AspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTyrCysThrGlyThr 514
Db 1771 GACTCAGCCATTGTCCACAGCTGCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1830
Qy 515 SerGlyGlyValLeuValCysGlnThrLysHisPheProTyrAlaAspGlyThrSerCys 534
Db 1831 CTCATGGCCATGCTGATGCTGACCAACAACTCGCCCTGGGCGGATGGCAGACCCCTGC 1890
Qy 535 GlyGluGlyLysTyrCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPhe 554
Db 1891 GGGCGCCGACACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950
Qy 555 AspThrProPheHisGlySerTyrGlyMetTyrGlyPheTyrGlyAspCysSerArgThr 574
Db 1951 AATATTCCAGGCTGGTGGGTCTTGGGACCAATGGGGTACTGCTCTCGGACC 2010
Qy 575 CysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGly 594
Db 2011 TGTGGGGTGGTGTCTCTCTCCGAGACTGACGAGGCGCTGTCCCCCGGAATGT 2070

Qy 595 GlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPro 614
Db 2071 GGCAAAGTACTGTGAGGCGCGGTACCGCTCTCGCTCTCTGCAACACTGAGGACTGCCCCA 2130
Qy 615 AspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSerLys 634
Db 2131 ACTGGCTCAGCCCTGACCTTCGGGAGGAGCAGTGTCTGCTACACCCAGCCAGCCAG 2190
Qy 635 AlaSerPheGlySerGlyProAla---ValGluTyrIleProLysTyrAlaGlyValSer 653
Db 2191 CTC---TTCAGAGCTTCCAGGCGCCCTGACTGGTCTCTGCTACACAGGCGGTGCC 2247
Qy 654 ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673
Db 2248 CCCAGGACAGTGCACAACTACCTGCCAGCCCGGCACTGGGCTACTACTATGTGCTG 2307
Qy 674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db 2308 GAGCCACGGGTGTAGATGGACCCCTGTTCCCGGACAGCTCTCGTCTGTGTCCAG 2367
Qy 694 GlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysPheAspLys 713
Db 2368 GCGCGATGCTATCCATGCTGTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2427
Qy 714 CysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleSerGlySerValThrSer 733
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Qy 734 AlaLysProGlyTyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluVal 753
Db 2488 TTCAGTACGATACCAATGTGTGCTACTATCCCGCGGGGCGCCACCATTCCTTGTGTC 2547
Qy 754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla 773
Db 2548 CGGACGAGGAAACCTTCGCCCGGAGC---ATCTACTTGGCCCTGAGCTGCCA 2601
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Db 2602 GATGCTCTCTATGCTCAATGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2661
Qy 794 TyrLysGlyValVal---LeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArg 812
Db 2662 CTGCTGGGGGAGTACGCTTCGCTCAGCGGGCCACTGCGAGCTCAGAGCTGCTGCTGCTG 2721
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Qy 853 ProThrPheSerAlaTyrVal-IleGluGlu---Tyr----- 863
Db 2839 CCCACTCCAGGAGTGGTGCACCGAAGAGCAGATTCCTGGAGATCTCTCGCGCGCGC 2898
Qy 864 ---GlyGluCysSer-----LysSerCys 870
Db 2899 CCCTGGCGCGGACAGAAATAACTCACTATCCCGGCTGCCCTTCTGGGCGACCCGGGCT 2958
Qy 870 sGluLeuGlyTyrGlnArg-----LeuValGluCysArgAspIleAsnGly 886
Db 2959 CGGACTAGCTGGGAGAAAGAGAGAGCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3018
Qy 886 yGlnProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs 906
Db 3019 GAGG-----GGCTGTGGCGTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3069
Qy 906 pHisProCysPro-----GlnTyrGln-----LeuGlyGluTyrSerSerCys 921
Db 3070 CTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3127

QY	535	GLYGLUGLYLSTP	CYSIL	ASNGLYLY	CYSVAL	ASNLYS	ASNHS	ARGLYSHIS	PHE	554
DB	1891	GGSCCCG	CACAGC	TGTCAT	GGGTGGT	CGCTGC	TCCACAT	GCACAC	GAGTCC	1950
QY	555	ASP	THR	PRO	PHES	IGLYSER	TRPGLY	MET	TRPGLY	574
DB	1951	AATATT	CCACAG	CGCTGG	TGGCTGGG	GCCTGG	GGGACCAT	GGGGT	GACTGCT	2010
QY	575	CYS	GLYGLY	VAL	GLN	TRP	MET	ARG	GLUCYS	594
DB	2011	TGTGGGGT	GGTGTCC	AGTTCT	CTCCCG	GAGACT	GCAC	CGAGGC	CTGTCCC	2070
QY	595	GLY	LYSTYR	CYS	GLUGLY	YSARG	VAL	ARG	SER	614
DB	2071	GGCAAG	TACTGT	CAGGGC	CGCCGT	TACCCG	GTCTCC	GTGC	AACACT	2130
QY	615	ASP	ASN	ASN	GLY	YS	THR	PHE	ARG	634
DB	2131	ACTGGCT	CAGCCCT	GACCTT	CCGCG	AGGAC	GAGT	GTCTGC	TACAC	2190
QY	635	ALA	SER	PHE	CYS	GLYSER	GLY	PRO	ALA	653
DB	2191	CTC---	TTCA	AGAGCT	TTCC	CAGG	CGCCAT	GGATGG	TGGTCT	2247
QY	654	PRO	LYS	ASP	ARG	CYS	LYS	LEU	ILE	673
DB	2248	CCCCAG	ACCAGT	CAACT	CACTGC	CCAG	CCCGGC	CACTGG	GGCTACT	2307
QY	674	GLN	PRO	LYS	VAL	VAL	ASP	GLY	THR	693
DB	2308	GAGCA	CGGTGG	TAGAT	GGGAC	CCCCGT	GTTC	CCCG	AACAGT	2367
QY	694	GLY	GLN	CYS	VAL	LYS	ALA	GLY	CYS	713
DB	2368	GGCCGAT	CAATCA	TGCTG	CTGTG	ATCG	CAATCG	CTTCC	AAGA	2427
QY	714	CYS	GLY	VAL	CYS	GLY	ASN	GLY	SER	733
DB	2428	TGCAT	GTGTG	CGGAG	GGGAC	GGTTCT	GGTTGC	AGCA	GAGT	2487
QY	734	ALA	LYS	PRO	GLY	TYR	HIS	ASP	ILE	753
DB	2488	TTCAGG	TACG	TACAC	AATAT	GTGGT	CACATAT	CCCC	CGGG	2547
QY	754	LYS	GLN	ARG	ASN	GLN	ARG	SER	ARG	773
DB	2548	CGGCAG	CAGG	GAAC	CCCTG	GC	CCAC	CGGAGC	-----	2601
QY	774	ASP	GLY	THR	TYR	ILE	LEU	ASN	GLY	793
DB	2602	GATGGCT	TCTCAT	TGCCCT	CANT	GTGTG	ATAC	AGCTG	ATG	2661
QY	794	TYR	LYS	GLY	VAL	VAL	---	LEU	ARG	812
DB	2662	CTGGCT	GGGCG	AGTC	AGCTT	CGCTAC	AGCGGG	GCAC	TCG	2721
QY	813	SER	PHE	SER	PRO	LEU	YS	GLUP	PRO	832
DB	2722	GGCCAT	GGCCACT	GGCC	CGCTT	GCAC	TCTG	AGTCTCT	AGTGG	2781
QY	833	ARG	PRO	LYS	ILE	YS	TYR	THR	PHE	852
DB	2782	GACAC	AGCCT	CCGAT	ACAGCTT	CTTC	GTG	CCCC	CGG	2838
QY	853	PRO	THR	PHE	SER	ALA	TRP	VAL	---	863
DB	2839	CCCACT	CCCC	AGGACT	GGCTGC	ACCG	AAGAC	ACAGAT	TTCTG	2898
QY	864	---	GLY	GLU	CYS	SER	---	---	---	870
DB	2899	CCCTG	AGCGG	GCAG	GAATA	ACCT	CACTAT	CCCG	GGCTGC	2958

Qy	870	SGLUeUGlyTrrGlnArg	-----LeuValGluCysArgAspIleasncl	886
Db	2959	CGGACCTTAGCTGGGAGAAAGAGAGACTTCTGTGTCTGCTGCTCATGCTAAGACTTCAGTGGG	3018	
Qy	886	YGINProAlaSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAs	906	
Db	3019	GAGG-----GGCTGTGGGCGTGAGACCTGCCCTCTCTCTGCCCTAATGCGAGG	3069	
Qy	906	pHisProCysPro-----GlnTrpGln-----LeuGlyGluTrpSerSerCysSe	921	
Db	3070	CTGGCCCTGCGCTGGTTCCTGCTCCCTGGGAGGAGTGATGGTGTAGTGGATGGAG--GG	3127	
Qy	921	rLysThrCysGlyLysGlyTyrrLysLysThrSerLeuLysCysLeuSerHisAspGlyG	941	
Db	3128	GCTGACAGACAGCCCTCCATAACTGCCCCCTCTGCCCCCTGCGGCTCACAGAGGGAGG	3187	
Qy	941	Y	941	
Db	3188	G	3188	
RESULT 11				
US-09-122-126B-14				
; Sequence 14, Application US/09122126B				
; Patent No. 6451575				
; GENERAL INFORMATION:				
; APPLICANT: Bristol-Myers Squibb Company				
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES				
; FILE REFERENCE: DM6909				
; CURRENT APPLICATION NUMBER: US/09/122,126B				
; CURRENT FILING DATE: 1998-07-24				
; NUMBER OF SEQ ID NOS: 21				
; SOFTWARE: PatentIn version 3.0				
; SEQ ID NO 14				
; LENGTH: 3250				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (121)..(2910)				
US-09-122-126B-14				
Alignment Scores:				
Pred. No.: 3,85e-164 Length: 3250				
Score: 1926.50 Matches: 400				
Percent Similarity: 53.53% Conservative: 123				
Best Local Similarity: 40.94% Mismatches: 325				
Query Match: 36.44% Indels: 130				
DB: 4 Gaps: 18				
US-09-373-658C-126 (1-967) x US-09-122-126B-14 (1-3250)				
Qy	5	ValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsnAlaGluArg-Al	24	
Db	156	GTTCGGCTGCTCCCTGCGCGC-----GGTCGGCCCCCGCCCGCAGC	194	
Qy	24	aProGlySerArgSerPheGlyProValProThrLeuLeuAlaAlaLeuLe	44	
Db	195	ACCTGCCCGAGATAAGCGGCGAGCTCGACT-----GCTGC	233	
Qy	44	uAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeuValProG	64	
Db	234	AGCAGCGCGCCAGCCCGCGCGGAGGAGGTGTCAGAGCGAGCCGAGCGCT--	291	
Qy	64	uLeuGluArgValProGlyHisGly-----ThrThrArgLeuArgLeuHisAlaPh	81	
Db	292	-----CCGGGTCACCCCGCACCCCTGCGCGAGCGCGCAGGAGCAAGGGGCT	338	
Qy	81	eAspGlnGlnLeuAsp-----	86	
Db	339	GGTGCAGAACTCATGCCAACTCTACTCCGCGCGCGCAAGGTGGGTACTCTGCTTACGC	398	
Qy	87	-----LeuAspValProProAspSerPheLeuAlaProGlyPh	100	

Db 399 GGGCGCGGAGGTTCTCTTGGACCTGGAGCGAGATGGTTCGGTGGCATTGCTGGCTT 458
QY 100 eThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLe 120
Db 459 CGTG-----CCCGAGAGCGCGGAGGAGTGGCCCTGGCGCCACCG 500
QY 120 uAlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSe 140
Db 501 GAGCCACTGCTTATCTATCGGGGACAGTGGACGCTAGTCCCGCTCTCTGCTGTCTTGA 560
QY 140 rLeuCysGluGlyValArgLysAlaPheTyLeuLeuGlyGluAlaTyPheIleGlnPr 160
Db 561 CTTCTGTGGGGGCTTCAGCGCTCTTTCGGGCTCAAGCAGCGCGCTACACCTAAAGCC 620
QY 160 oLeu-----ProAlaAlaSerGlu-----166
Db 621 ACTGTCGCGGACCTTGGCGCGAGGAAGAAAGGCGCGGTGTACGGGATGGGTCCGC 680
QY 167 ArgLeu-AlaThrAla-----Alap 173
Db 681 ACGGATCTCTGACGCTCTACACCGCGAGGCTTCAGCTTCGAGCGCCTCGCGCGCGCG 740
QY 173 rcGlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyA 193
Db 741 CAGCTCGGAACCCCGCGCTCA-----763
QY 193 spValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGluT 213
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QY 213 hrGluAspGluAspGluGlyThrGluGlyLysGluGlyProGlnTpsrProGlnA 233
Db 792 GC-----ACAGCAACCGGCGGAGCGCGGACACTGG---CCTCGCA 830
QY 233 spProAlaLeuGlnGlyValGlyGlnProThrGlyThr-----GlySerI 248
Db 831 GCTCTTGGACCACTGCTCTCTCGCGCGCTCGGGGCTCAGGACCGCAGACGTGGTGGCG 890
QY 248 leArgLysLysArgPheValSerHisArgTyValGluThrMetLeuValAlaAspG 268
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QY 268 lnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyLeuLeuThrLeuPheSerV 288
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QY 288 alAlaAlaArgLeuTyLysHisProSerIleArgAsnSerValSerLeuValValVal 308
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Db 1070 AGTGTGGTGTAGGCGACAAGGACAGAGCTGGNAGTGAGCAAGNAGCTGCCACCA 1129
QY 328 hrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaG 348
Db 1130 CACTCAAGAACTTTTGAAGTGGCAGCACCAACACCAACACCACTGCGGAGATGACCATGAG 1189
QY 348 lchHisTyAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysA 368
Db 1190 AGCACTACGAGCAGCTATCTGTTACTCGGAGGATTTATGTGGCATCATTCATGTG 1249
QY 368 spThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSerValI 388
Db 1250 ACACCTTGGGAATGGCAGAGCTTGGGACCATATGTTCTCCAGAGCGCAGCTGTGCTGA 1309
QY 388 leGluAspAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPhea 408
Db 1310 TTGAAGACGATGGCCTCCAGCGAGCCTTCACTGTGGCTCAGAAATCGGACATTTACTTG 1369
QY 408 snMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerH 428
Db 1370 GCCTCTCCGATGAGATTCCAATCTCTGTGAGAGACCTTTGGTTCCACAGAGATAAGC 1429

QY 428 isMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerG 448
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QY 468 lnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyAspAlaAsnArgLnc 488
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QY 488 ysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSer 508
Db 1610 GCAACCTGACATTCGGGCTGAGTACTCGGTGTGCC---GGCATGGATGCTGTGCTC 1666
QY 508 hrLeuTrpCysThrGlyThrSerGlyValValCysGlnThrTyHisPheProT 528
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QY 528 rpAlaAspGlyThrSerCysGlyGluGlyLysTyPheCysIleAsnGlyLysCysValAsnL 548
Db 1727 CGGTGGAAGGAGCGCTTGTGAAAGGGGAGAACTCGCTCGAGGGCAATGTGTGGACA 1786
QY 548 ysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyProT 568
Db 1787 AAACCAAGAAATAATATTATTCAGCTCAAGCCATGGCACTGGGGATCTTGGGGATCCT 1846
QY 568 rpGlyAspCysSerArgThrCysGlyGlyValGlnTyThrMetArgGluCysAspA 588
Db 1847 GGGGCGAGTGTCTCGCTCATGTGGAGGAGGAGTGCAGTTTTCCTATCTGCTCACTGTAATA 1906
QY 588 snProValProLysAsnGlyGlyTyPheCysGluGlyLysArgValArgTyArgSerC 608
Db 1907 ACCCTGCTCCCAAGAACACGACGCTCTGTGACAGGGAAGAGGCCATCTACCGCTCCT 1966
QY 608 ysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluA 628
Db 1967 CAGTCTCATGCTGCCGCCACCC---AATGCTAAATCATTTGCTCATGAACAGTGTGAGG 2023
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Db 2024 CAAATAATGGCTATCAGTCTGATGCAAAAGGAGTCAAACTTTTGTGGATGGTTCCCA 2083
QY 648 yTyTyAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleG 668
Db 2084 AATATGCAAGTGTCTCGCCAGCGGATGTGTGCAAGCTGACCTGCAGAGCCAAAGGCACTG 2143
QY 668 lyTyPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerT 688
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QY 708 ysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIleS 728
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QY 728 erGlySerValThrSerAlaLysProGlyTyThrHisnspIleIleThrIleProThrGlyA 748
Db 2324 TTGGAAACCTTTAATAAGAAAAGTAAAGGGTTACCTGACGTGGTGAGGATTCCTGAGGGG 2383
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Db 2384 CAACCCACATAAAGTTCGACAGTTCARAGCCAAAGACCAGACTAGATTCACTGCCTATT 2443
QY 768 euAlaIleLysAlaAlaAspGlyThrTyTrpIleLeuAsnGlyAspTyThrLeuSerThrL 788
Db 2444 TAGCCCTGAAAGAAAACCGGTGATCTTATCAATGGAAGTACATGATCTCCACTT 2503

QY 388 leGluAspGlyLeuGlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheA 408
DB 1310 TTGAAGACGATGGCTCCAGCAGCTTCACTGTGCTCAGGAATCGGACATTTACTTG 1369
QY 408 snMetProHisAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerH 428
DB 1370 GCTCTCCCATGAGATTCGAATTCGTGAAGAGACCTTTGGTTCCACAGAGAATAAGC 1429
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DB 1490 CAGCCACCATCAGAGAATTCCTGGATGGCCATGTAACCTGTTTCTGGACCTACAC 1549
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QY 488 ysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCysSerT 508
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QY 528 rpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnL 548
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QY 568 rpGlyAspCysSerA-gThrCysGlyValGlnTrpThrMetArgGluCysAspA 588
DB 1847 GGGGCGAGTGTCTCTCTATGTGGAGAGAGAGTGTGCTATGCTATGCTATGTAATA 1906
QY 588 snProValProLysAsnGlyLysTyrCysGluGlyLysArgValA-gTyrArgSerC 608
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QY 608 ysAsnLeuGluAspCysProAspAsnGlyLysThrPheArgGluGlnCysGluA 628
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QY 648 ysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleG 668
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QY 668 lyTyrPheValLeuGlnProLysValValAspGlyThrProCysSerProAspSerT 688
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QY 688 hrSerValCysValGlnGlyCysValLysAlaGlyCysAspArgIleIleAspSerL 708
DB 2204 ATTCCGCTCTGCTCGCGGGAAGTGTGTGAGAACTGGCTGTGACGCGCATCAATGGCTCAA 2263
QY 708 ysLysLysPheAspLysCysGlyValCysGlyValAsnGlySerThrCysValLysLys 728
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QY 894 ysGluValLysProAlaSerThrArgProCysAlaAspHisProCys 909
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RESULT 13
US-09-369-364A-1
; Sequence 1, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3002
; TYPE: DNA
; ORGANISM: mus musculus ADAMTS-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2810)
US-09-369-364A-1

Alignment Scores:
Pred. No.: 1,17e-162 Length: 3002
Score: 1909.50 Matches: 393
Percent Similarity: 56.83% Conservative: 127
Best local Similarity: 42.95% Mismatches: 314
Query Match: 36.12% Indels: 82
DB: 4 Gaps: 19

US-09-373-658C-126 (1-967) x US-09-369-364A-1 (1-3002)

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Qy 470 oIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPhe 490
Db 1352 CTACCCCTTTGGCTGCTCAACTGCCAGGCATCCTTTACACAGTGAATAACAATGGAAT 1411
Qy 490 eThrPheGlyGluAspSerLysHisCysProAspAlaAsnThrCysSerThrLeuTr 510
Db 1412 GATTTTGCACAGGTTCTCAGGTGCGCCA---TATATGATGCAGTCGACAGGCTCTG 1468
Qy 510 pCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAs 530
Db 1469 GTGCAATACGTCATGAGTACACAAAGGCTGCCGACTCAGCACACACCCCTGGGCCGA 1528
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Db 1529 TGGACGGAGTGGAGCCTGGAAAGCACTGCAAGNATGATTTGTGT--- 1577
Qy 550 sArgLysHisPheAspThrProPhe---HisGlySerTrpGlyMetTrpGlyProTrpG 569
Db 1578 -CCCAAGAAATGCGATGCTCCCGTGACAGATGATCCTGGGAAGTGGAGTCCCTTTGG 1636
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Db 1697 AGAACCAAAATGTTGGAATATCTGTGTAGGACGTAGATGAATTTAACTTCTGCA 1756
Qy 609 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHi 629
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Qy 629 sAsnGluPheSerLysAlaSerPhe-----GlySerGlyProAlaValGluTrpI 646
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Qy 646 eProLysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysG 666
Db 1865 CCTATAATACAGTGAATTTCTGATGAAGACCGGTGCAAGTGTGTTCTGCAGAGTGGCAGG 1924
Qy 666 yIleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAs 686
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Qy 686 pSerThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleLeAs 706
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Qy 706 pSerLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLy 726
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Qy 766 rPheLeuAlaIleLysAlaAspGlyThrTrilleLeuAsnGlyAspTyrThrLeuSe 786
Db 2225 CTACTTAGCTTATCAGCAGTAAGGTGATCTTCTGCTTAATGGAACACTTGTGTGTAC 2284
Qy 786 rThrLeuGluAsnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAl 806

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Qy 806 aAlaLeuGluArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLe 826
Db 2345 TGCGGTAGAAGAAATTAACCTCAACAGATGCGATTGACGAAAGAACTTTTGCTTCAGGTTT 2404
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Db 2465 TAAACCTCAGCAGTTTTTACTGGAACAGTCATGCGCCATGGCAAGCATGCACTAAACCC 2524
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Qy 857 ----- 857
Db 2765 GGTGTGATGATGTTTTTGCACAGCCATCCCAACCAAGCAACCGTGAATAATGCTCAGG 2824
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Db 2825 GGAATGTAACACGGGTGGCTGCTGCTATCTGCTGAGTGAATGTTCAAAAAGCTGTGA 2884
Qy 871 uLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGln-----ProAl 889
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Db 2945 CAGCAATGCAACATCAGAGAAAGTTCACATTCAGAGG---TGCACTGAGTTCCTTG 3001
Qy 909 sProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLy 929
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Qy 949 pProLeuLysLysProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
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RESULT 15

US-09-369-364A-14
; Sequence 14, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirschata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 28473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369.364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14

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? LENGTH: 2625
? TYPE: DNA
? ORGANISM: Mus musculus ADAMTS-9
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (2)..(2623)
US-09-369-364A-14

Alignment Scores:
Pred. No.: 6,73e-136 Length: 2625
Score: 1613.00 Matches: 341
Percent Similarity: 55.99% Conservative: 145
Best Local Similarity: 39.29% Mismatches: 312
Query Match: 30.51% Indels: 71
DB: 4 Gaps: 26

US-09-373-658C-126 (1-967) x US-09-369-364A-14 (1-2625)

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Db 8 GCGGTCAATCAGCTGTCTCGGAATGATGGCAGCAGCTTCGGCTCTCACGATGGAGATTAT 67
QY 157 PheIleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLys 176
Db 68 TTCATTGAACACCTGCAGCTCTGTGGATGAGAA-----GAGGATGAAGAGAA 115
QY 177 ProProAlaProLeuGlnPheHisLeuLeuArgArgAsn-----ArgGlnGly 192
Db 116 CAAACAAACCC-----CACATTATTATAGGCACAGCAGCCCTCAGAGGGAACCC 166
QY 193 AspValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGlu 212
Db 167 TCCACGGAAGAACGATGCTGTGCACCTCAGAACTCAAAAATAGTCACAGTAAGA-CAA 225
QY 213 ThrGluAspGluAspGluGlyThrGluGlyGluAsp----- 224
Db 226 GCGGAATAATCAGATGCGAAACCGAGAGAGAGGAAATAGCTGCTGACGAGCTGGCACT 285
QY 225 -----GluGlyProGlnTrpSerProGlnAspProAlaLeuGln 237
Db 286 GCTAAAGAGCGGTTTGGCAACAAAGGTCTCTCTGGCTATAGCAA-----CAGACAAACAA 342
QY 238 GlyValGlyGlnProThrGlyThr-GlySerIleArgLysLysArgPheValSerSerHi 257
Db 343 CACAGGGACAG-----ATGGAACCAACAAAGAACCAAGCGCTTCTGTCTCTACC 393
QY 257 sArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerG1 277
Db 394 ACAGTTGTAGAGGTGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 453
QY 277 yLeuLysHisIstYrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSe 297
Db 454 CTTTCAACATTATATCTTACCTTAATGTCTTATGTCTTATGTCTTATGTCTTATGTCTTATGT 513
QY 297 rIleArgAsnSerValSerLeuValValLysIleLeuValIleHisAspGluGlnLys 317
Db 514 TATTGGAATTTAATTAATATTGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 573
QY 317 sGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys 337
Db 574 AGGACCTTACATAATTTCAATGTCCACACACATTAAGAAGCTTTTCCAGTGGCAGCA 633
QY 337 sGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheTh 357
Db 634 CTCAAAGAAC-----TACTTGGTGGGATTTCAGCACACAGCGGTTCTGGTCAC 684
QY 357 rArgGlnAspLeuCysGlySerGln---ThrCysAspThrLeuGlyMetAlaAspValG1 376
Db 685 AAGGGAAGATATCTGCAGAGCTCAGACAAATGTGCACACCTTAGTCTCTGTGTAAGTGGG 744
QY 376 yThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAl 396
Db 745 AACCAATTTCGACCCCTACCGAGCTGTCTTCCATTAGTGAAGACAGTGGGCTGAGCACAGC 804
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Db 805 TTTCAATAGCTCAGAGCTGGCCATGTGTTTAAATATGCTCAGCATGACAGCAATAA 864
QY 416 nCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAs 436
Db 865 ATGCAAGAA---GAAGGAGTTAAGAGTCCCAGCATGTCATGGCCACCAACACTGAATTT 921
QY 436 nLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAs 456
Db 922 CTACACCAACCCCTGGATGTGTCAAAGTGCACTCGGAATAATACATCACTGAGTTCTCTAGA 981
QY 456 pAsnGlyHisGlyGluCysLeuMetAspLysPro---GlnAsnProIleGlnIleuProG1 475
Db 982 CACTGGGTACGGAGAGTGTCTGCTGAATCAACCTGCATCCAGGACCTATCTCTTTCCTTTC 1041
QY 475 yAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAs 495
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Db 1102 CTCTCAAGTGTGCCCC---TATATGATGCACTGAGCAGCGCTCTGCTGCAATAATGTGGA 1158
QY 515 rGlyGlyValLeuValCysGlnThrLysHisPheProGlnAlaAspGlyThrSerCysG1 535
Db 1159 TGGAGCACAAAGGCTGCAAGACTCAGCACAGCCCTGGGCAGATGGAAACCCAGTGTGA 1218
QY 535 yGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAs 555
Db 1219 GCCTGGAAGACCTGCAAGTTTGGATTGTGTGT-----CCCAAGAAATGGA 1266
QY 555 pThrPro---PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgTh 574
Db 1267 GGCCCTCTCAATTTGATGATGCTCTGGGAGGTTGGAGCCACTTTGGGACCTCTCAAGAAC 1326
QY 574 rCysGlyGlyGlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnG1 594
Db 1327 GTGTGGAGGAGCATCAAAACAGCCATCAGAGAGTCCAAACAGACAGAGCCAAATAATGG 1386
QY 594 yGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysPr 614
Db 1387 TGGGAAGTACTGTGTAGGAAGGAGAAATGAAGTTTCAATCTCTGCAACCGAGAGCCCTGCAT 1446
QY 614 oAspAsnAsnGlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLy 634
Db 1447 GAAGCAGAG---CGAGACTTCCAGAGAGGAGAGTGT---GCTCAC-----TTTGATGG 1494
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QY 651 yValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePh 671
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QY 671 eValLeuGlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCy 691
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QY 691 sValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSerLysLysLysPh 711
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Db 2035 GAACGTGACGGACCGTATCAGGAGAACTTCTCCTTCAGGTGTGTCCGTGGGAAAGCT 2094
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Db 2095 GTATAACCCAGATGCGGTACTCTATTCAATATTCCTATGAGGACAACTCAGCAATT 2154
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QY 888 oAlaSerGlu-----CysAlaLysGluValIysProAlaSer---ThrArgProCysAl 905
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Job time : 292.321 secs

GenCore version 5.1.6
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Run on: June 18, 2004, 18:42:30 ; Search time 947.831 Seconds
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Title: US-09-373-658C-126

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Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	5287	100.0	4014	11	US-09-989-687-125	Sequence 125, Appl
2	5232	99.0	4014	15	US-10-115-286-1	Sequence 1, Appli
3	5232	99.0	4014	14	US-10-105-929-1	Sequence 1, Appli
4	5224	98.8	4309	15	US-10-210-120-57	Sequence 57, Appl
5	5224	98.8	4459	16	US-10-159-563-192	Sequence 192, Appl
6	5224	98.8	4459	16	US-10-159-563-308	Sequence 308, Appl
7	5224	98.8	4760	10	US-09-971-429B-17	Sequence 17, Appl
8	5144	97.3	3261	10	US-09-373-658-1	Sequence 1, Appli
9	5144	97.3	3261	11	US-09-989-687-1	Sequence 1, Appli
10	5140.5	97.2	4848	13	US-10-425-114-46851	Sequence 26851, A
11	4287	81.1	4878	12	US-10-152-319A-1840	Sequence 1840, App
12	4287	81.1	4878	16	US-10-191-803-170	Sequence 170, Appl
13	4277.5	80.9	4180	10	US-09-373-658-20	Sequence 20, Appl
14	4277.5	80.9	4180	11	US-09-983-687-20	Sequence 20, Appl
15	3922	74.2	2184	9	US-09-445-023A-2	Sequence 2, Appli
16	3922	74.2	2184	15	US-10-097-587-2	Sequence 2, Appli
17	3922	74.2	2184	15	US-10-097-580-2	Sequence 2, Appli
18	3652	69.1	2184	9	US-09-445-023A-13	Sequence 13, Appl
19	3652	69.1	2184	15	US-10-097-597-13	Sequence 13, Appl
20	3652	69.1	2184	15	US-10-097-580-13	Sequence 13, Appl
21	3411	64.5	9248	10	US-09-373-658-21	Sequence 21, Appl
22	3411	64.5	9248	11	US-09-989-687-21	Sequence 21, Appl
23	3303	62.5	3477	9	US-09-803-589-1	Sequence 1, Appli
24	2642	50.0	3145	9	US-09-803-589-9	Sequence 9, Appli
25	2498.5	47.3	2804	16	US-10-093-463-27	Sequence 27, Appl
26	2496	47.2	3446	9	US-09-965-631-7	Sequence 7, Appli
27	2478.5	46.9	2937	13	US-10-275-107-24	Sequence 24, Appl
28	2478	46.9	2853	9	US-09-965-631-3	Sequence 3, Appli
29	2474	46.8	2867	13	US-09-741-151-1	Sequence 1, Appli
30	2461	46.5	2930	17	US-10-311-035-32	Sequence 32, Appl
31	2334	44.1	3715	13	US-10-425-114-46850	Sequence 26850, A
32	2332.5	44.1	3711	17	US-10-283-975A-398	Sequence 398, App
33	2331.5	44.1	3008	10	US-09-373-658-3	Sequence 3, Appli
34	2331.5	44.1	3008	11	US-09-989-687-3	Sequence 3, Appli
35	2271.5	43.0	3638	9	US-09-918-171A-8	Sequence 8, Appli
36	2208.5	41.8	2940	14	US-10-163-316-1	Sequence 1, Appli
37	2190.5	41.4	2469	14	US-10-163-316-3	Sequence 3, Appli
38	2161	40.9	4307	13	US-10-358-283-31	Sequence 31, Appl
39	2161	40.9	4307	16	US-10-191-937-121	Sequence 121, Appl
40	2156	40.8	4192	15	US-13-247-685-1	Sequence 1, Appli
41	2149	40.6	4407	10	US-09-946-374-316	Sequence 316, App
42	2149	40.6	4407	12	US-10-015-395A-316	Sequence 316, App
43	2149	40.6	4407	13	US-10-206-915-351	Sequence 351, App
44	2149	40.6	4407	13	US-10-199-670-351	Sequence 351, App
45	2149	40.6	4407	13	US-10-201-858-351	Sequence 351, App

ALIGNMENTS

RESULT 1
US-09-989-687-125
; Sequence 125, Application US/09989687
; Publication No. US2004000249A1

GENERAL INFORMATION:

; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven W.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1480.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 125
; LENGTH: 4014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (466)..(3366)
; OTHER INFORMATION:
US-09-989-687-125

Alignment Scores:

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-989-687-125 (1-4014)

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QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAnglyLysThr 620
DB 2266 AAACGAGTGGCTACAGATCTCTTAACCTTGGAGCTGTCCACACATATATGGAACCAAC 2325
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2326 TTTAGAGAGAACATGTGAGGACACACAGAGTTTCAAAAGCTTCTTTGGAGTGGG 2385
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2386 CTTGCGGTGGATGGATTCACAGTACGCTGGCGTCTCCACAAAGGACAGGTGCAAGCTC 2445
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValAlaAspGly 680
DB 2446 ATCTGCCAAGCCAAAGGCAATGGCTACTTCTTCTGTTTTCAGCCCAAGGTGTAGATGGT 2505

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Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2506 ACTCCATGTAGCCAGATTCACCTCTGTCTGTGCAAGACAGTGTGTAAAGCTGGT 2565
Qy 701 CysAspArgIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2566 TGTGATCGCATCATAGATCCAAAGAGATTTGATAAATGTGTTTCCGGGGGAAT 2625
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2626 GGATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTCAAAACCTGGATATCATGAT 2685
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2686 ATCATCAATTCACCTGAGGACCAACATCGAGTGAACAGCGAACCCAGAGGGGA 2745
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
Db 2746 TCCAGGAACAATGGCAGCTTCTTGCCATCAAGCTGCTGATGCCACATATATCTTAAT 2805
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2806 GGTGACTACACTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGTGCTTTGAGG 2865
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2866 TACAGGGCTCTCTCGGCAATGGAAAGATTCGCAGCTTTAGCCCTCTCAAGAGCCC 2925
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2926 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTGCACCTAAATTAATACACCTAC 2985
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaIleValIle 860
Db 2986 TTGTAAGAGAGAGAGAGAGATTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3045
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3046 GAAGAGTGGCGCGCAATCTTCTAAGTCATGTGAATTCGGTGGCAGAGAACTGGTAGAA 3105
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TCCCGAGACATTAATGACAGCTGTCTTCCGATGTGCAAAAGAGTGAAGCAGCCAGC 3165
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGCAGACCATCTCTGCCCCAGTGGCAGCTGGGGAGTGGTCATCATGT 3225
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3226 TCTAAGACCTGTGGGAAGGTTTACAAAAAACCAAGCTTGAAGTGTCTGTCCCATGATGA 3285
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGACAGCTGTGATCTTTTAAAGAACCTTAAACATTTATAGACTTT 3345
Qy 961 CysThrMetAlaGluCysSer 967
Db 3346 TGCACAATGGCAGATGCACT 3366
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RESULT 2

US-10-115-286-1

; Sequence 1, Application US/10115286

; Publication No. US20030166065A1

; GENERAL INFORMATION:

; APPLICANT: Jonak, Zdenka

; Trulli, Stephen

; Forwald, James

; Terratt, Jonathan

; Hastings, Gregg

; TITLE OF INVENTION: No. US20030166065A1el Integrin Ligand ITGL-TSP

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

```
ADDRESSEE: Ratner & Prestia
STREET: Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,286
FILING DATE: 04-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,496
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4014 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-115-286-1

Alignment Scores:
Pred. No.: 0 Length: 4014
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 15 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-115-286-1 (1-4014)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 466 ATGCGAGCGAGCTGTGCCCGAGGGGTTCGGAAGCGCAAGCTGGCGAGCATGGGGNAC 525
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 526 GCGGAGCGGGCTCCGGGGTCTCGAGCTTTGGGCGCGTACCCACAGCTGCTGTCTGCTCGCC 585
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 586 GCGGCGCTACTGGCGGTGTTCGACCACTTCGGGCGCCCTCCAGAGAGGACGAGGACTA 645
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 646 GTGGTGGCGGAGCTGGAGCGCGCCCGCGGACACGCGGCTCCGCTGCGCAGCC 705
Qy 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 706 TTGTACACGACGCTGGATCTGGGCGCGCCCGGACAGAGCTTTTGGCGCGCGGCTTC 765
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 766 ACGCTCCAGACGTCGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAACCCGACCTG 825
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 826 GCGCAGCTCTTACTCCGGCACCGTGAATGGCGATCCAGCTCGGCTCGCGCCCTCAGC 885
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QY 141 LeuCysGluGlyValAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 886 CTCGCGAGGCGTGGCGGCGCCCTTCTACCTGTGGGGAGGGGTATTTTCATCCAGCGG 945
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
DB 946 CTGCCGCGCGCAGGAGCGCTCGCCACCGCGCCCGGAGAGAGCGCGGCGACCA 1005
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
DB 1006 CTACAGTTTCCACTCTCTCGCGCGGAATCGGAGGCGGACGTAGGCGGCGACGTGGCGGGGTC 1065
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 1066 GTGACGACGAGCGCCCGCGCCACTGGGAAGCGGAGACCGGAGCGAGCGGAGGACT 1125
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1126 CAGGCGGAGGACGAGGCGCTCAGTGTGGCGGAGGACCGGCACTGCAAGGCGGTAGGA 1185
QY 241 GlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHisArgTyrVal 260
DB 1186 CAGCCACAGAACTGGAGGACATAGAAAGAGCGATTGTTCAGTCCAGCCGTATGTG 1245
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1246 GAAACCATGCTGTGGCAGACCGAGTCGATGGCAGATTCCACGCGCAGTGTCTAAAGCAT 1305
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
DB 1306 TACTCTTCACGTTGTTTCGGTGGCAGCCAGATTGTACAAACACCCCGCAGCATTCGTAA 1365
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
DB 1366 TCAGTTAGCTGTGTGGTGAAGATCTGTGTCTCCACGATGACAGAGGSGCCGGA 1425
QY 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
DB 1426 GTGACCTCCAAATGTCCTCACTCTCGGGAACCTTTGCAACTGCGAGAAGCAGCAAC 1485
QY 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
DB 1486 CCACCCAGTGACCGGATGACAGACATATGACACAGCAATCTTTTCCACGACAGGAC 1545
QY 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
DB 1546 TTGTGTGGGTCCACACATGTGATCTCTGGGATGGCTGATGTGGAACCTGTGTGTAT 1605
QY 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrAla 400
DB 1606 CCGAGCAGAAGCTGCTCCGTATAGAAGATGATGTTTACAGCTGCTTCCACACAGCC 1665
QY 401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
DB 1666 CATGAATTAGCCAGCTGTTTAAACATGCCATGATGATGATGATGATGATGATGATGAT 1725
QY 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
DB 1726 AATGTGTGAACACAGAGTCCACATGATGGCGTCAATGCTTTTCAACCTGGACACAGC 1785
QY 441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
DB 1786 CAGCCTTGTCTCTCTGTCAGTGCCTACATGATTACATCTTCTCGATAATGGTCATGGG 1845
QY 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
DB 1846 GAAATCTTGTGAGGACAAGCCTCAGAAATCCATACAGCTCCCGAGCGCATCTCCCTGGCACC 1905
QY 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
DB 1906 TCGTACGATGCCAACCGGAGTGCAGGTTTACATTTGGGAGGACTCCCAACACATCGCCT 1965

QY 501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
DB 1966 GATGCGAGCCAGCATGATGTAGCACCTTGTGTGTGTACCGGCACCTCTGTGTGGGTGCTGTGTG 2025
QY 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
DB 2026 TGTCAAAACCAACACATTCCTCGTGGGGGATGGCCAGCTGTGGAGAAGGAATGTGTGT 2085
QY 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
DB 2086 ATCAACGCGCAAGTGTGTGAACAAACCGACAGAAAGCATTTGTATACGCTTTTCATGGA 2145
QY 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyGlyValGln 580
DB 2146 AGCTGGGGAATGTGGGGCTTGGCGAGACTGTTCGAGAACGTGCGGTGGAGGATCCAG 2205
QY 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGlyGly 600
DB 2206 TACACGATGAGGAATGTGACAAACCCAGTCCCAAGATGGAGGAGTACTGTGAAGGC 2265
QY 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
DB 2266 AATGAGTGGCTACAGATCTCTTAACCTTGAGGACTGTCCACACAATAATATGAAGAAC 2325
QY 621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
DB 2326 TTTAGAGAGAAACAATGTGAAGCACACAACGAGTTCCTCAAAAGCTTCCTTTGGAGTGGG 2385
QY 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
DB 2386 CTGCGGTGGAAATGGATTCCCAAGTACGTGGGCTCTCACCAAGGACAGGTGCAAGCTC 2445
QY 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
DB 2446 ATCTGCAAGCCAAAGCATTTGGCTACTTCTCTGTTTTCAGGCCCAAGGTGTAGATGGT 2505
QY 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyClnCysValLysAlaGly 700
DB 2506 ACTCCATGTAGCCAGATCCACTCTGTCTGTGTGCAAGACAGTGTGTAAAGCTGT 2565
QY 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
DB 2566 TGTGATCGCATCATAGACTCCAAAAGAGATTGTGATAAATGTGTGTTCGCGGGGAAAT 2625
QY 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
DB 2626 GGAATCTACTTGTAAAAAATATCAGGATCAGTTACTAGTGTCAAAACCTGGATATCATAT 2685
QY 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
DB 2686 ATCATCACAATTCCACTGGAGCCCAACATCGAAGTGAACAGCGGAACACAGAGGGA 2745
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
DB 2746 TCCAGGAACAATGGGAGCTTTCTTGGCATCAAAAGCTGCTGATGGCAGATATATCTTAAT 2805
QY 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
DB 2806 GGTGACTACACTTTGTTCACCTTAGAGCAAGACATATATGTACAAAGGTGTGCTTGAGG 2865
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
DB 2866 TACAGCGCTCTCTCGGCAATTTGGAAGAAATTCGAGGCTTTAGCCCTCTCAAGAGGCC 2925
QY 821 LeuThrIleGlnValLeuThrValGlyAspAlaLeuArgProLysIleLysTyrThrTyr 840
DB 2926 TTGACCATTCAGGTTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2985
QY 841 PheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
DB 2986 TTCGTAAGGAAGAAGGAATCTTTCAATGTCTATCCCACTTTTTCAGCATGGTCAAT 3045
QY 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880

Db 3046 GAGAGTGGCGCGAAGTCTTAAGTCAATGTAATGGTTGGCAGAGAACTGGTAGAA 3105
Qy 881 CyeArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3106 TGGCGAGACATTAATGACAGCGCTCTCCGAGTGTGCAAGAGAGTGAAGCCAGC 3165
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3166 ACCAGACCTTGTGAGACCACTCCCTGCCCGCAGTGGCGAGTGGGGAGTGGTCATGT 3225
Qy 921 SerLysThrCysGlyLysGlyLysLysLysLysLysLysLysLysLysLysLysLys 940
Db 3226 TCTAAGACCTGTGGCAAGGTTTCAAAAAGAGAGCTTGAAGTGTCTGTCCCTGATGGA 3285
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3286 GGGGTGTATCTCATGAGAGTGTGATCTCTTAAAGAAAGCTTAAACATTTTCATAGACTTT 3345
Qy 961 CysThrMetAlaGluCysSer 967
Db 3346 TGCACAATGGCAGAATGAGT 3366

RESULT 3

US-10-105-929-1
; Sequence 1, Application US/10105929
; Publication No. US20020137142A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/10105,929
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (460)...(3360)
US-10-105-929-1

Alignment Scores:
Pred. No.: 0 Length: 4676
Score: 5232.00 Matches: 957
Percent Similarity: 99.38% Conservative: 4
Best Local Similarity: 98.97% Mismatches: 6
Query Match: 98.96% Indels: 0
DB: 14 Gaps: 0

US-09-373-658C-126 (1-967) x US-10-105-929-1 (1-4676)

Qy 1 MetClnArgAlaValProGluGlyPheGlyArgArgGlyLysLeuGlySerAspMetGlyAsn 20
Db 460 ATGCAGCGAGCTGTGCCCGAGGGGTTCGGAAGCGCGAAGCTGGCGACGACATGGGGGAC 519
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 520 GCGAGAGGGGCTCCGGGGTCTCGAGAGCTTGGGGCCGTAACCCAGCTGCTGCTGCTGCC 579
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 580 GCGCGGCTACTGGCGGTGTGCGAGCGCTCGGGCGCCCTCCGAGGAGGACGAGGAGCTA 639

Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 640 GTGGTCCCGAGCTGAGCGCGCCCGGACACCGGACACCGCCCTCCGCTCGACGCC 699
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Db 700 TTGACACAGCTGAGTGTGAGCTGCGCCCGACAGCAGCTTTTGGCGCCCGGCTTC 759
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
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Qy 121 AlaHisCysPheTySerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 820 GGCATCTGCTTCTACTCCGCGACCGGTAATGGCATCCAGCTCGGCTCGCCCGCTCAGC 879
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 880 CTCTCGAGGGGTGCGCGCGCTTCTACTGCTGGCGGAGCGCTATTTCATCCAGCCG 939
Qy 161 LeuProAlaAlaSerClnuArgLeuAlaThrAlaAlaProGlyClnuLysProProAlaPro 180
Db 940 CTGCCCGCGCAGCGAGCGCTCGCCCGCGCCCGCGCGGAGAGCGCGCGGACCA 999
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Db 1000 CTACAGTTCCACTCTCTCGCGGAAATCGGACGGGCGAGTAGCGGCGCTCGGGGTC 1059
Qy 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 1060 GTGACGACGAGCGCGCGCGCTGGAAGAGCGGAGCGAGCGAGGAGCGAGGAGGACT 1119
Qy 221 GluGlyLysAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 1120 GAGGCGAGGACGAGAGGGCTCTAGTGTGTCGCCAGGACCGGCACTGCAAGCGTAGGA 1179
Qy 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
Db 1180 CAGCCACAGGAACCTGGAAGCATAAGAAAGAGCGATTTGTGTCCAGTACCGCTATGTG 1239
Qy 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1240 GAAACCATGCTGTGGCAGACCGAGTCGATGGCGAGAATTCACGCGAGTGTGTAAAGCAT 1299
Qy 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
Db 1300 TACCTTCTACGTTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCAGCATTCGTAT 1359
Qy 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1360 TCAGTTAGCTGTGTGTGTAAGATCTTGGTCATCCAGATGAACAGAGGGCGCGAA 1419
Qy 321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
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Qy 341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
Db 1480 CCACCCAGTGACCGGATGACAGACACTATGACACAGCAATCTTTTTCACACACAGGAC 1539
Qy 361 LeuCysGlySerClnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1540 TTGTGTGGGTCCAGACATGTGATCTTGTGGATGGCTGTGATGTGGAACTGTGTGTGAT 1599
Qy 381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
Db 1600 CCGAGCAGAAGCTGCTCCGTCATAGAAGATGATGTTTACAAGCTCCCTTCCACACAGGCC 1659
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
Db 1660 CATGAATTAGGCGACCGTGTTTTAACTGATGATGATGATGATGATGATGATGATGATG 1719
Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440

Db 1720 AATGGTGTGAACAGGATTTCCACATGATGGCGTCAATGCTTTTCCAACTGACACACAGC 1779
Qy 441 GlnProTyrSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
Db 1780 CAGCCTTGCTCTCCTTGCAGTGCCTACATGATTAATCATTTCTGATGATGGTCAATGG 1839
Qy 461 GluCysLeuMetAspIleProGlnAsnProIleGlnLeuProGlyValLeuProGlyThr 480
Db 1840 GAATGTTTGTATGGACCAAGCCTCAGAAATCCATACAGCTCCCAAGGCGATCTCCCTGGCAC 1899
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerIleHisCysPro 500
Db 1900 TCGTACGATGCCAACCGGCGAGTGCCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCC 1959
Qy 501 AspAlaIleSerThrCysSerThrIleuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
Db 1960 GATGACGACGACATGATGACACCTTGTGGTGTACCGGACCTCTGGTGGGGTGTGGTG 2019
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2020 TGTCAACCAACACACTTCCCGTGGCGGATGGACACGCTGTGGAGAGGGAATGGTGT 2079
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
Db 2080 ATCAACGGCAAGTGTGAACAAACCGACACAAAGACATTTTGATACGCTTTTTCATGGA 2139
Qy 561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
Db 2140 AGCTGGGAAATGTGGGGCCTTGGGAGACTGTTCCAGAACTGTCGGTGGAGGAGTCCAG 2199
Qy 581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGluGly 600
Db 2200 TACACGATCAGGGAATGTGACACACCGTCCCAAGAAATGGAGGGAAGTACTGTGAAGGC 2259
Qy 601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnGlyLysThr 620
Db 2260 AAACGAGTGGCTCAGATCTGTAACTTGGAGACTGTCCAGAAATGGAGGGAAGTACTGTGAAGGC 2319
Qy 621 PheArgGluGlnGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
Db 2320 TTTAGAGAGGAAACATGTGAAGCACACACAGAGTTTTCAAAGACTTCTTTGGGAGTGGG 2379
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysIleLeu 660
Db 2380 CCTGGGTGGATGGATTTCCCAAGTACGCTGGCGTCTCACCACCAAGGACAGGTGTAGATGT 2439
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2440 ATCTGCCAAGCAAGGCAATGGCTACTTCTCGTTTTCAGCCCAAGGTTGTAGATGT 2499
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2500 ACTCCATGTAGCCAGATTCACCTCTGCTGTGTGCAAGGACAGTGTGTAAAGCTGGT 2559
Qy 701 CysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCysGlyValAsn 720
Db 2560 TGTGATGCCATCATAGACTCCAAAAGAGTTTGTATAATGTGGTGTGGGGGAAT 2619
Qy 721 GlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2620 CGATCTACTGTGAAAAAATATCAGGATCAGTTACTAGTGCACAAACCTCGATATCATGAT 2679
Qy 741 IleIleThrIleProThrGlyValThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2680 ATCATACAAATTCACATGGAGCCCAACATCGAAGTGAACACAGCGGAACAGAGGGGA 2739
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAspGlyThrTyrIleLeuAsn 780
Db 2740 TCCAGGAACAAATGGCAGCTTTCTGCCATCAAGGCTGTGTGTCGACATATATTTCTTAAT 2799
Qy 781 GlyAspTyrThrLeuSerThrIleuGlnAspIleMetTyrLysGlyValLeuValLeuArg 800

Db 2800 GGTGACTACACTTTGTCCACTTAGACCAAGACACATTATGTACAAAGGTGTGTCTTGAGG 2859
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2860 TACAGCGCTCCTCTGGCGCATTCGAAAGAAATTCGAGCTTTAGCCCTCTCAAGAGGCC 2919
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2920 TTGACCATCCAGGTTCTTACTGTGGCAATGCCCTTCGACTAAATTAATATACACCTAC 2979
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2980 TTCGTAAGAGAGAAAGAAATCTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 3039
Qy 861 GluGlnTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 3040 GAAGATGGGGCGAATGTTCTAGTCAATGGAATGGGTGGCAGAGAACTGGTAGAA 3099
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 3100 TCCGAGACATTAATGACACAGCTGCTTCGAGTGTCAAAGGAAGTGAAGCCAGCCAGC 3159
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 3160 ACCAGACTTGTGACAGCACTCCCTGCCCGAGTGGAGCTGGGGAGTGTGTATCATGT 3219
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3220 TCTAAGACCTGTGGGAAGGGTTCAAAAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGA 3279
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3280 GGGGTGTATCTCATGAGAGCTGTGATCTTTAAAGAAACCTAAACATTTTCATAGATTT 3339
Qy 961 CysThrMetAlaGluCysSer 967
Db 3340 TGCACAAATGACAGATGCAGT 3360
RESULT 4
US-10-210-120-57
; Sequence 57, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UN-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 4309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-57
Alignment Scores:
Pred. No.: 0 Length: 4309
Score: 524.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 15 Gaps: 0
US-09-373-658C-126 (1-967) x US-10-210-120-57 (1-4309)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20

116 ATGACGCGAGCTGTGCGCGGGGTTCCGAGAGCGCGCAAGCTGGCGAGCAGCATGGGGAGC 175
21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
176 GCGGAGCGGGCTCCGGGTCTCGAGCTTTGGGCCAGTACCCAGCTGTGTCTGCTCGCC 235
41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
236 GCGGCGCTACTGGCGGTCTCGAGCGACTCGGGCGGCCCTCCGAGGAGGACGAGGAGCTA 295
61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
296 GTGCTGCGGAGCTGAGCGCGCCCGGAGACCGGACACCGGCGCTCCGCTGCGCCGCGC 355
81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
356 TTGACGAGCAGCTGAGCTGGAGCTCGGCCCGCGAGCAGAGCTTTTGGCGCCCGGCTTC 415
101 ThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGluThrAspLeu 120
416 ACGCTCCAGAACCTGGGGCGCNAATCCGGGTCCGAGAGCGCGCTTCGGGAACCGGACCTG 475
121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
476 GCGCACTGCTTACTCCGCGACCGTGAATGGCGATCCCAAGCTCGGCTCGCGCCCTCAGC 535
141 LeuCysGluGlyValArgGlyAlaPheThrLeuLeuGlyGluAlaThrPheLeuGlnPro 160
536 CTCTCGAGGGCGTGGCGCGGCTTCTACTGCTGGGGAGGCGGTATTTTCAATCCAGCGG 595
161 LeuProAlaAlaSerGluArgGluAlaThrAlaAlaProGlyGluLysProProAlaPro 180
596 CTCGCGCGCGCAGAGCGGCTCGCACCGCGCGCCCGAGGGAGAGCGCGCGGACCA 655
181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal 200
656 CTACAGTTCCACTCTCTCGCGCGGAATCGGAGGCGAGCTCGCGCGGCGAGTGGGGGTC 715
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
716 GTGACGACGAGCGCGCGGCTGGGAAAGCGAGACCGAGACGAGGACGAGGAGGACT 775
221 GlnGlyGluAspGluGlyProGlnThrSerProGlnAspProAlaLeuGlnGlyValGly 240
776 GAGGGCGAGGACGAGGCGCTCAGTGTGTGCGCGCAGGACCGCGCACTGCAAGCGTAGGA 835
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
836 CAGCCCGACAGAACTGGAGCATAAGAAAGACGGAATTTGTGTCCAGTCACCGCTATGTG 895
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
896 GAAACCATGCTTGTGGCAGACCATGATGGCAGAAATTCACGGCAGTGTCTTAAAGCAT 955
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
956 TACCTTCTCAGCTGTGTTCGGTGCGAGCGAGATGTACAAACACCCCGCATTCGTAAT 1015
301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
1016 TCAGTTAGCTGTGTGTGGTGAAGATCTTGTCATCCACCATGAAACAGAAAGGGCGGAA 1075
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnThrProGlnLysGlnHisAsn 340
1076 GTCACTTCCAAATGCTGCGCTCATCTGCGGAATTTTGCACACTGGCAGAGCAGCAAC 1135
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
1136 CCACCCAGTGACCGGATGACAGACACTATGACACAGCAATTTCTTTCACCGACAGGAC 1195
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380

1196 TTGTGTGGTGTCCAGACATGTGATACTCTTTGGGATGGGTGATGTTGGAACTGTGTGTGAT 1255
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
1256 CCGAGCAGAGGTGCTCCGTGATGAAGATGATGTTTACAAGTGCCTTCCACAGCC 1315
401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
1316 CATGAATAGGCCACGTGTTTAAACATGCCACATGATGATGATCAAGCAGTGTGCCACCTT 1375
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1376 AATGTGTGAACAGGATTTCCACATGATGGGTCAATGCTTTTCCAACTGGACCAAGC 1435
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1436 CAGCCTTGTCTCTCTTGCAGTGCCTACATGATTAATCATTTCTGGATTAATGGTCATGG 1495
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1496 GAATGTTTGTATGGACAAGCTCAGAAATCCCATACAGTCCCAAGCGATCTCCCTGGCACC 1555
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1556 TGTGATGATGCCAACCGCGAGTGCAGATTTACATTTGGGAGAGCTCCAAACACTGCCCC 1615
501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
1616 GATGAGCCGAGCACATGTAGCACCTTGTGTGTACCGGCACCTCTGGTGGGTGCTGGTG 1675
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
1676 TGTCAAAACCAACACTTCCCGTGGCGGATGGCACAGCTGTGGAGAGGAAATGGTGT 1735
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
1736 ATCAACGCGCAGTGTGTGAACAAACCGACAGAAAGCATTTTGTATACGCTTTTTCATGA 1795
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
1796 ACGTGGGAATGTGGGCGCTTGGGAGACTGTTCCAGAACGTGGCGTGGAGAGTCCAG 1855
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysLysTyrCysGluGly 600
1856 TACACATGAGGAAATGTGACAAACCATGTCACCAAGATCGAGGAGNAGTACTGTGAAGC 1915
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
1916 AAACGAGTGGCTACAGATCTCTGTAACTTGAGGACTGTCCAGACAATTAATGGAACCC 1975
621 PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
1976 TTTAGAGAGAAACAATGTGAACACACACAGAGTGTTCAAAAGCTTCTTTGGAGTGGG 2035
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2036 CCGTGGTGAATGATTTCCCAAGTACGTCGCGCTCACCAAAAGCAGAGGTGCAAGCTC 2095
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2096 ATCTGCCAAGCAAGGATTTGGCTTCTTCTGTTTTCAGCCCAAGTGTGTAGATGGT 2155
681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
2156 ACTCAATGATAGCCAGATTTCCACTCTGTCTGTGTGCAAGGACAGTGTGTAAAGCTGT 2215
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2216 TGTGATCGCATCATAGACTCCAAAAAAGAGTTTGAATAATGTGTGTTTTCGGGGGAAAT 2275
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2276 GGATCTTACTTGTAAAAAATAATATCAGATCAGTTACTTAGTGCAAAACCTTGGATATCATGAT 2335

QY 741 lleileThrIleProThrGluAlaThrAenilleGluValLysGlnArgAspGlnArgGly 760
Db 2336 ATCAATCAAAATCCAACTGGAGCCACCAACATCGAAGTGAACACGCGAACAGAGGGA 2395
QY 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrlleLeuAsn 780
Db 2396 TCCAGGAACAATGGCAGCTTTCTGCCATCAAGCTGCTGATGGCACATATATTCTTAAT 2455
QY 781 GlyAspTyrlleLeuSerThrLeuGluGlnAspIleMetTyrlleValLysGluValLysArg 800
Db 2456 GGTGACTACACTTTGTCCACCTTAGACGAAGCATATATGACAAAGGTGTGTCTTGAGG 2515
QY 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2516 TACAGCGGCTCTCTGCGCATTTGGAAGATTCGACGCTTTAGCCCTCTCAAGAGGCC 2575
QY 821 leuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrlleThr 840
Db 2576 TTGACCATCCAGGTCTTACTGTGGCAATGCGCTTCGACCTTAATAATTAAATACACCTAC 2635
QY 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaIleValle 860
Db 2636 TTCTGTAAGAAGACAGAGAACTTTTCAATGCTATCCCACTTTTTCAGCATGGGTCAAT 2695
QY 861 GluGluThrGlyGluCysSerLysSerCysGluLeuGlyThrGlnArgArgLeuValGlu 880
Db 2696 GAAGAGTGGGGCAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGACTGGTAGAA 2755
QY 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2756 TCCAGAGACATTAATGGACAGCTGCTTCGAGTGTGCAGAGGATGAGCCAGCCAGC 2815
QY 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2816 ACCAGACCTTGTGCAGACCATCCCTGCCCGCCAGTGGCAGCTGGGGAGTGGTCAATCAT 2875
QY 921 SerLysThrCysGlyLysGlyTyrlleLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 2876 TCTAAGACTGTGGGAAGGTTTACAAAAGAAAGCTTGAAGTGTCTGTCCCATGATGGA 2935
QY 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 2936 GGGGTGTTATCTCATGAGAGCTGTGATCCTTTAAAGAAACCTTAAACATTTTCATAGACTT 2995
QY 961 CysThrMetAlaGluCysSer 967
Db 2996 TGCACAAATGGCAGATGCAGT 3016

RESULT 5

US-10-159-563-192
; Sequence 192, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; FILE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 4459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-192

Alignment Scores:
Pred. No.: 0 Length: 4459
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservative: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 16 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-192 (1-4459)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgGlyLysLeuGlySerAspMetGlyAsn 20
Db 243 ATGCGAGGAGCTGTGCCGAGGGGTTCCGAAGGCCGCAAGCTGGCGACGACATGGGGAC 302
QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 303 GCGCAGCGGCTCGGGGCTCTCGGAGCTTTGGGCGCGTACCCACGCTGCTGCTGCTGCC 362
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluGluLeu 60
Db 363 GCGCGCTACTGCGCGCTGTCCGACGCACTCGGGCGCCCTCCGAGGAGGAGGAGGACTA 422
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 423 GTGGTGGCGGAGCTGGAGCGCGCGCCCGGACACGCGACCAACGCGCTCCGCTCGACGCC 482
QY 81 PheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe 100
Db 483 TTTGACGAGCAGCTGTGAGTCTGGAGCTCGCGCCGACGACGAGCTTTTGGCGCCCGGCTTC 542
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 543 ACGCTCCAGAACGTGGGGCGCAATCCGGGTCCGAGACGCGCTTCGGAACACCGACCTG 602
QY 121 AlaHisCysPheTyrlleSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 603 GCGCAGCTGCTTCTACTCCGCGACCGTGAATGGCGATCCAGCTCGGCTGCGCCCTCAGC 662
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrlleLeuLeuGlyGluAlaTyrlleGlnPro 160
Db 663 CTCTGCGAGGGCGTGGCGCGCGCTTCTACTGCTGGGGAGGCGTATTTTCATCCAGCG 722
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 723 CTGCCCCCGCGCAGCAGCGCTCGCCACCGCCCGCCCGAGGGAGAGCGCCCGGACCA 782
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyTyrlleCysGlyVal 200
Db 783 CTACAGTTCCACCTCTCTGCGCGGGAATCGGCGAGGCGACGTCGCGCGCACGTCGCGGCTC 842
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
Db 843 GTGACGCGAGCCCGCGCGCTGCGAAAGCGGAGACCGAAGACGAGGACGAGAGGAGT 902
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
Db 903 GAGGCGAGGAGCAAGGGGCTCAGTGTGCGCGCAGACCGCGGCTGCAAGGCGTAGGA 962
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrlleVal 260
Db 963 CAGCCACAGGAACCTGGAGCATTAAGAAGCGATTGTGTCTCAGTCCAGCTATGTG 1022
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
Db 1023 GAAACCATGCTTGTGGCAGACCACTCGATGCGAGAAATTCACGAGTGTCTTAAGCAT 1082
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrlleLysHisProSerIleArgAsn 300
Db 1083 TACCTTCTCAGTTGTTTTCGTTGGCAGCCAGATTGTACAAACACCCAGCATTCGTAAT 1142
QY 301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1143 TCAGTTAGCTGTGGTGGTGAAGATCTTGTGTCATCCACGATGAACAGAGGGCGCGGAA 1202

321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
1203 GTGACCTCCAAATGCTGCCCTCACTCTCGGAACTTTTGCAACTGGCAGAGCAGCAAC 1262
341 ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
1263 CCACCCAGTGCAGGAGTGCAGAGCACTATGACACAGCAATCTTTTCCACAGCAGGAC 1322
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
1323 TTGTGTGGTCCACAGACATGTGATCTCTTGGATGGCTCATGTGGAACTGTGTGTGAT 1382
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaIlePheThrTrpAla 400
1383 CCAGCAGAGAGCTGCTCCGTCATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1442
401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
1443 CATGAATTAGGCCACAGTGTTTTACATGCCACATGATGATCAAAAGCAGTGTGCCAGCCTT 1502
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1503 AATGGTGTGAACAGGATTCCTCATATGATGGCTCAATGCTTTCCAACTGGACACAGC 1562
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1563 CAGCCTTGGTCTCTTCGAGTGCCTACATGATTTACATCAATCTCTGGATAATGTCATGGG 1622
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1623 GAATGTTTGTATGGACAAGCCCTCAGAATCCCATACAGCTCCAGGCGATCTCCCTGGCACC 1682
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
1683 TCGTACGATGCCAACCGGAGTGCATTTACATTTGGGGAGGACTCCAAACACTGCCCC 1742
501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
1743 GATGACCCAGCACATGATGACCTTGTGGTGTACCGGACCTCTGGTGGGGTGTGCTGGT 1802
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
1803 TGTCAAAACCAACACTTCCCGTGGCGGATGCGACAGCTGTGGAGAGGAAATGTTGT 1862
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560
1863 ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCATTTTGATACGCTTTTCATGGA 1922
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
1923 AGCTGGGGAATGTGGGGGCTTGGGGAGCTGTTCCGAAAGCTGCGGTGGAGGAGTCCAG 1982
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyrCysGluGly 600
1983 TACACGATGAGGGAATGTACAAACCCAGTCCCAAGAAATGGAGGAAGTACTGTGAAGC 2042
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
2043 AAACGAGTGCCTACAGATCCTGTAACTTGGAGACTGTCAGACAAATAATGGAAAAACC 2102
621 PheArgGluGlnCysGluAlaHisArgGluPheSerLysAlaSerPheGlySerGly 640
2103 TTTAGAGAGGAACAAATGGAAGCAACACAGGTTTTCAAAAGCTTCTTTGGAGTGGG 2162
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2163 CCTGGGTGGAATGGAATTCCTCCCAAGTAGCTGCTCCCTCACCAAGCAGCAGGTGCAAGCTC 2222
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2223 ATCTGCCAAGCAAGGATTTGGCTACTTCTTCTGCTTTTGCAGCCCAAGGTTGTAGATGGT 2282

681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
2283 ACTCCATGTAGCCCAAGATTCCACCTCTGTCTGTGTCAAGGACAGTGTGTAAAGCTGT 2342
701 CysAspArgIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
2343 TGTGATCGCATCATGACTCCAAAAGAGATTGTATAAATGTGGTGTTCGGGGGGAAT 2402
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2403 GGATCTACTTTGTAAAAAATATCAGATCGATCTAGTGTCAAAACCTGGATATCATGAT 2462
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
2463 ATCATCACAAATTCCAACTGGAGCCCAACATCGAAGTGAAGTGAAGCCAGAGAGCGGA 2522
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
2523 TCCAGGAACAATGGCAGCTTTCTTGCATCAAAAGCTGTGTGTGCACATATATCTTTAAT 2582
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2583 GGTGACTACACTTTGTCACCTTAGAGCAAGACATTTATGTACAAAGGTGTGTCTTGAG 2642
801 TyrSerGlySerSerAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
2643 TACAGCGGCTCTCTCGCGCATTTGGAAAGAAATTCGCAGCTTTAGCCCTCTTCAAGAGCCC 2702
821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
2703 TTGACCATTCAGTTCCTTACTGTGGCCANTGCCCTTCGACCTAAATTAATACACCTAC 2762
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
2763 TTCGTAAGAAGAAAGAAATCTTTCAATGCTATATCCCACTTTTTCAGCATGGGTCAAT 2822
861 GluLysTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
2823 GAAGAGTGGCGGCAATTTCTAAGTCAATGTGAATTCGGTTCGCAGAGAGACTGTGTAGAA 2882
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
2883 TGCCGAGACATTAATGGACAGCTGCTTCCGAGTGTCAAAAGAAAGTGAAGCCAGCCAGC 2942
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
2943 ACCAGACCTTGTGCAGACCATCTCCCTCCCTCAGTGCAGCTGGGGAGTGTCTCATGT 3002
921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
3003 TCTAAGACCTGTGGGAAGGTTTACAAAAAAGAAAGCTTGAAGTGTCTGTCCCATGTGA 3062
941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
3063 GGGGTGTATCTCATGAGAGCTGTGATCTCTTAAGAAACCTTAACATTTTCATAGACTTT 3122
961 CysThrMetAlaGluCysSer 967
3123 TGCACAATGGCAGATGCACT 3143

RESULT 6

US-10-159-563-308
; Sequence 308, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563

; CURRENT FILING DATE: 2002-12-09
 ; PRIOR APPLICATION NUMBER: US 10/133,937
 ; PRIOR FILING DATE: 2002-04-25
 ; NUMBER OF SEQ ID NOS: 444
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 308
 ; LENGTH: 4459
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-159-563-308

Alignment Scores:

Pred. No.: 0 Length: 4459
 Score: 5224.00 Matches: 956
 Percent Similarity: 99.28% Conservative: 4
 Best Local Similarity: 98.86% Mismatches: 7
 Query Match: 98.81% Indels: 0
 Ds: 16 Gaps: 0

US-09-373-658c-126 (1-967) x US-10-159-563-308 (1-4459)

QY	1	MetGlnArgAlaValProGluGlyPheGlyArgArgGlyLeuGlySerAspMetGlyAsn	20
DB	243	ATGCGAGCGAGCTGTGCCCCAGGGGTTTCGGAAGCGCGAAGCTGGCGAGCGACATGGGGAAC	302
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla	40
DB	303	CGGGAGCGGGCTCGGGGGTCTCGGAGCTTTGGGCCGCTACCCACGCTGCTGCTCGCC	362
QY	41	AlaAlaLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu	60
DB	363	GGGGCGCTACTGGCGGTGTGCGAGCGACCTCGGGCGCCCTCCGAGGAGGACGAGAGCTA	422
QY	61	ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla	80
DB	423	GTGGTGGCGGAGCTGAGCGCGCCCGGACACGCGGACACCGCGCTTCGCGCTCGCGCC	482
QY	81	PheAspGlnLeuAspLeuAspValProProAspSerSerPheLeuAlaProGlyPhe	100
DB	483	TTTGACCGACGCTGGATCTGGAGCTCGCGCGCCGACGAGAGCTTTTGGCGCGCGGCTTC	542
QY	101	ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu	120
DB	543	AGCTCCAGAACGTGGGGGGCGAAATCCGGGTTCGAGACGCCCTTCGCGAAGACCGACCTG	602
QY	121	AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer	140
DB	603	CGGCACTGCTTCTACTCCGGCACCGTGAATGGCATCCCGAGCTCGCTCGCGCCCTCAGC	662
QY	141	LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro	160
DB	663	CTCTGGAGGGCGGTGGCGCGCGCTTCTTACCTGCTGGGGGAGCGGATTTTCATCCAGCGG	722
QY	161	LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProAlaPro	180
DB	723	CTGCCCGCGCGCAGCGAGCGCTCGCCACCGCGCGCCCGCAGGGGAGAGCGCGCGACCA	782
QY	181	LeuGlnPheHisLeuLeuArgAsnArgGlnGlyAspValGlyGlyThrCysGlyVal	200
DB	783	CTACAGTCTCCCTCTCTGGCGGGGAATCGCGAGGGCGACGTGCGGGCGCACGTGCGGGGTC	842
QY	201	ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr	220
DB	843	GTGGAGCAGCGAGCCCGCGCGAGCTGGGAAGCGGAGACCGAGAGCAGGACGAGGGACT	902
QY	221	GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly	240
DB	903	GAGGGCGAGACGAGAGGGGCTCAGTGGTGGCGCGCGCAGGACCCCGGCACTGCAAGCGGTAGGA	962
QY	241	GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal	260
DB	963	CAGCCCAACAGGAATCGAAGCATAGAAAGACCGGATTTGTTCAGTCCCGCTATGTG	1022

QY	261	GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis	280
DB	1023	GARACCATGCTGTGGCAGACCATGATGGCAGAAATCCACGGCAGTGGTCTTAAGCAT	1082
QY	281	TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn	300
DB	1083	TACCTTCTCAGTGTGTTTTCGGTGGCAGCCAGATTGTACAAACACCCCGCAGCATTCGTAAT	1142
QY	301	SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu	320
DB	1143	TCAGTTAGCTGGTGGTGGTGAAGATCTTGCTCATCCACGATGAACAGAAAGGGCGCGAA	1202
QY	321	ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn	340
DB	1203	GTGACCTCCAAATGCTGCCCTCCTCTCGGAACTTTTGCAACTGGCAGAGCAGCACAAC	1262
QY	341	ProProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp	360
DB	1263	CCACCCAGTGCACCGGATGCAGACACTATGACACAGCAATTTCTTTTCCACAGACAGAC	1322
QY	361	LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp	380
DB	1323	TTGTGTGGTCCCAGACATGTGATPACTCTTGGGATGGCTGATGTGTGAACTGTGTGAT	1382
QY	381	ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla	400
DB	1383	CCGAGCAGAAAGCTGCTCCGTATAGAAGATGATGGTTTACAAGCTGCCCTTCCACACAGCC	1442
QY	401	HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu	420
DB	1443	CATGAATTAGGCCACCGTGTTTAATCATGCCACATGATGCAAGAGCATGTGCCAGCTTT	1502
QY	421	AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer	440
DB	1503	AATGGTGAACACAGGATTCACACATGATGGCGTCAATGCTTTCCAACTGGACACACAGC	1562
QY	441	GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly	460
DB	1563	CAGCTTGTGCTCTCTTCAGTGCCTTACATGATTAATCATTTCTGGATAATGGTCATGGG	1622
QY	461	GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr	480
DB	1623	GAATGTTTGTATGGACAGCCTCAGATCCCATACAGCTCCACAGCGCATCTCCCTGGCAC	1682
QY	481	SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro	500
DB	1683	TCGTACGATGCAACCGCGCAGTGCCTTACATTTTGGGGAGGACTCCAAACACTGCCCTC	1742
QY	501	AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal	520
DB	1743	GATGCGCCAGCACATGTAGCACTTGTGTGTATACCGGCACCTCTGGTGGGGTGTGTGTG	1802
QY	521	CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys	540
DB	1803	TGTCAAAACCAACACTTCCCGTGGCGGATGGCACCTGCTGTGGAGGAAGGAATGGTGT	1862
QY	541	IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly	560
DB	1863	ATCAACGGCAAGTGTGTGAACAAACCGACAGAAAGCAATTTTGATACGCCCTTTTCATCGA	1922
QY	561	SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln	580
DB	1923	AGCTGGGGAATGTGGGGGCTTGGGGAGACTGTTCGAGAACGTGCGTGGAGGAGTCCAG	1982
QY	581	TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTrpCysGluGly	600
DB	1983	TACAGATGAGGGGAATGTGACCAACCCAGTCCCAAGAAATGAGGGAAGTACTGTGAAGGC	2042
QY	601	LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr	620
DB	2043	AAACGAGTGGCTACAGATCCTGTAACTTGGAGGACTGTCCAGACAAATAATGGAAGAAC	2102
QY	621	PheArgGluGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly	640

Db 2103 TTATAGAGAGCAAAATGTGAAGCACACACAGAGTTTTCAAAAGCTTCCTTTGGGAGTGGG 2162
Qy 641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
Db 2163 CCGTGGGTGGATGGATCCCAAGTACGCTGGGTCTCCACAAAGGACAGGTGCAAGCTC 2222
Qy 661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
Db 2223 AFTGCGCAAGCCAAAGGCAATGGCTACTCTCTCGTTTTCAGGCCCAAGGTGTGAGATGT 2282
Qy 681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
Db 2283 ACTCCATGTAGCCCAAGATCCACCTCTGCTGTGTGCAAGGACAGTGTGTAAGCTGCT 2342
Qy 701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyGlyAsn 720
Db 2343 TGTGATCGCATCATAGACTCCAAAGAAAGTTGTATAATGTGTCTTCGCGGGGAAT 2402
Qy 721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
Db 2403 GGATCTACTGTGAATAAATATACGATCATGTTACTAGTGCACAAACCTGGATATCATGAT 2462
Qy 741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
Db 2463 ATCATCACATTCCACTGGAGCCACCAACATCGAAGTGAACAGCGGAACACAGAGGGA 2522
Qy 761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrIleLeuAsn 780
Db 2523 TCAGGAGCAATGGAGCTTCTTGCCATCAAGCTGCTATGGCACATATATCTTAAT 2582
Qy 781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
Db 2583 GGTGACTACACTTGTCCACCTTAGACAGACATATGTACAAAGGTGTGTTCTTGAGG 2642
Qy 801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
Db 2643 TACAGCGGCTCTCTCGGCAATGGAAAGAAATTCGACGCTTTAGCCCTCTCAAGAGCCC 2702
Qy 821 LeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLysTyrThrTyr 840
Db 2703 TTGACCATCCAGGTCTTACTGTGGCAATGCCCTTCGACCTAAATTAATACACCTAC 2762
Qy 841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
Db 2763 TTGCTAAAGAAAGAAAGGAATCTTTCAATCTCTATCCCCACTTTTTCAGCATGGGTCAIT 2822
Qy 861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
Db 2823 GAAGAGTGGGGCGAATGTTCTAAGTCATGTAATTTGGTTGGCAGAGACACTGCTAGAA 2882
Qy 881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
Db 2883 TGCAGACATTAATGACAGCCTGCTTCGAGTGTGCAAGGAAGTGAAGCAGCAGCAGC 2942
Qy 901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920
Db 2943 ACCAGACCTTGTGAGACCAATCCCTGCCCCAGTGGCAGCTGGGGAGTGGTTCATGAT 3002
Qy 921 SerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSerHisAspGly 940
Db 3003 TCTAAGACCTGTGGAGAGGTTACAAAAAAGAGCTTTGAAGTGTCTGTCCTCCATGATGA 3062
Qy 941 GlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPheIleAspPhe 960
Db 3063 GGGGTGTATCTCATGAGCTGTGATCTTTTAAAGAAACCTAAACATTTTCATAGACTTT 3122
Qy 961 CysThrMetAlaGluCysSer 967
Db 3123 TGCACATGGCAAGATGAGT 3143

RESULT 7

US-09-971-429B-17

; Sequence 17, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 4760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 007074.13
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
; US-09-971-429B-17

Alignment Scores:
Pred. No.: 0 Length: 4760
Score: 5224.00 Matches: 956
Percent Similarity: 99.28% Conservatives: 4
Best Local Similarity: 98.86% Mismatches: 7
Query Match: 98.81% Indels: 0
DB: 10 Gaps: 0

US-09-373-658C-126 (1-967) x US-09-971-429B-17 (1-4760)
Qy 1 MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn 20
Db 561 ATGCAGCAGCTGTGCCGAGGGTTCCGAGGCGCAAGCTGGGAGGACACATGGGGAAC 620
Qy 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
Db 621 GCGGAGCGGGCTCCGGGGTCTCGGAGCTTTGGGCCAGTACCCACGCTGCTGCTCGCC 680
Qy 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
Db 681 GCGGCGCTACTGCGCGTGTGCGACGCACTCGGCGCGCCCTCCGAGGAGACGAGGAGCTA 740
Qy 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
Db 741 GTGGTGCCGAGCTGGAGCGCCCGGACACGAGACCCAGCGCTCGGCTTCAGCGCC 800
Qy 81 PheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAlaProGlyPhe 100
Db 801 TTTGACACGACGCTGGATCTGGAGCTGGGCGCCGACAGCAGCTTTTGGCGCCCGGCTTC 960
Qy 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
Db 861 AGCTTCCAGAACGTGGGGGCAAAATCCGGGTCCGAGACGCCGCTTCCGGAAACCGACCTG 920
Qy 121 AlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
Db 921 GCGCACTGCTTCTACTCGGCACTGGATGGAATGGCGATCCAGCTCGGCTCGGCTTCAGC 980
Qy 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
Db 981 CTCTCGAGCGGTGCGCGCGCTTCTACCTGCTGGGGAGGCGGTATTTTCATCCAGCG 1040
Qy 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysProProAlaPro 180
Db 1041 CTGCGCGCGCGCGAGGCGCTTCGCCACCGCGCGCCCGGAGGAGAGCGCGCGGCAACA 1100

181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlnGlyAspValGlyThrCysGlyVal 200
1101 CTACAGTTCCACTCTCTGGGGCGGATCGCGAGGCGAGCTAGGCGGCGACGTCGGGCTC 1160
201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
1161 GTGGACGACGAGCCCGCGCGACTGGGAAGCGGAGACCGAGACGAGGAGCGAGGACT 1220
221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
1221 GAGGCGAGGACGAGGAGGCTCAGTGGTCGCGCGAGGACCCGCACTCGACGGCGTAGGA 1280
241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerHisArgTyrVal 260
1281 CAGCCACAGGAACCTGGAAGCATAGAAAGAGAGCGATTGTCTCCAGTCACCGCTATGTG 1340
261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
1341 GAACCATCTCTGTGGCAGACCGATCGATGGCAGAAATTCACCGCAGTGGTCTAAGCAT 1400
281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
1401 TACCTTCTCACGTTGTTTGGTGGCAGCCAGCATTTGTACAAACACCCCGCAGCATTCGTAAT 1460
301 SerValSerLeuValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
1461 TCAGTTAGCTGGTGGTGGTGAAGATCTTGGTCATCCAGATGAAACAGAGGGGCGGAA 1520
321 ValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
1521 GTGACCTCAATGCTGCTCACTCTCGCGAACTTTTGCAACTGGCAGAGCAGCACAA 1580
341 ProProSerAspAspAlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAsp 360
1581 CCACCCAGTCAGCGGAGTGCAGAGCACTATGACAGCAATTTCTTTTCCACGACAGGAC 1640
361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
1641 TTGTGTGGTCCGACACGATGATCTCTTGGATGGCTGATGTTGGAACTGTGTGAT 1700
381 ProSerArgSerCysSerValIleGluAspAspGlyLeuGlnAlaAlaPheThrThrAla 400
1701 CCGACGAGAAGCTGCTCCGCTCATAGAAGATGATGTTTACAGCTGCTTCCACACAGCC 1760
401 HisGluLeuGlyHisValPheAsnMetProHisAspAlaLysGlnCysAlaSerLeu 420
1761 CATGAATTAGGCCACGCTGTTTAACTATGCCATGATGATGATGCAAGCATGTGCCAGCTT 1820
421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
1821 AATGGTGTGAACACGAGATTCCACATGATGGGCTCAATGCTTTTCCAACTGGACACAGC 1880
441 GlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGly 460
1881 CAGCTTGTGCTCTCTTGACGTGCTTACATGATATCATTTCTGGATAATGGTCATGGG 1940
461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
1941 GAATGTTTGTAGACAAAGCCTCAGAAATCCATPACAGCTCCCGAGCGATCTCCCTGGCA 2000
481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
2001 TCGTACGATGCCAACCGGAGTGCAGTTACATTTGGGAGGACTCCAAACACTGCCCC 2060
501 AspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGlyValLeuVal 520
2061 GATGACGACGACATGTAGCACTTGTGTGTACCGGCACCTCTGGTGGGCTGTGGTG 2120
521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
2121 TGTCAAAACAAACACTTCCCGTGGGCGATGGCAGCATGGTGGAGAGGAAATGTTGT 2180
541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrProPheHisGly 560

2181 ATCAACGCGCAAGTGTGTGAACAAACCCAGACAGAAAGCATTTTGATACGCTTTTCATGGA 2240
561 SerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGlyValGln 580
2241 AGCTGGGGAATGTGGGGCCTTGGGAGACTGTTTCGAGAAGCTGCGGTGAGGAGTCCAG 2300
581 TyrThrMetArgGluCysAspAsnProValProLysAsnGlyGlyLysTyrCysGlyGly 600
2301 TACACGATGAGGAATGTGACCAACCCAGTCCCAAGAATGGAGGGAAGTACTGTGAAGGC 2360
601 LysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThr 620
2361 AAACGATGGCTACAGATCTGTAACTTTGAGGACTGTCCAGACAATAATGGAAAAAC 2420
621 PheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPheGlySerGly 640
2421 TTTAGAGAGGAACAATGTGAAGCACACAACGAGTTTTTCAAAAGCTTCTTTGGGAGTGGG 2480
641 ProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArgCysLysLeu 660
2481 CCTCGGTGGAATGATTCACAGTACGCTGGCGTCTCCACAAAGGACAGGTGCAAGCTC 2540
661 IleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysValValAspGly 680
2541 ATCTGCCAACCCAAAGGCATTTGGCTACTTCTCGTTTTCAGCCCAAGTTGTAGATGT 2600
681 ThrProCysSerProAspSerThrSerValCysValGlnGlyGlnCysValLysAlaGly 700
2601 ACTCCATGTAGCCAGATTCACCTCTGTCTGTGTGACAGACAGTGTGTAAAAAGCTGGT 2660
701 CysAspArgIleIleAspSerLysLysPheAspLysCysGlyValCysGlyValAsn 720
2661 TGTGATCGCATCATAGACTCCAAAGAGAGTTGATTAATGTGTGTGTTTGGCGGGAAAT 2720
721 GlySerThrCysLysLysIleSerGlySerValThrSerAlaLysProGlyTyrHisAsp 740
2721 GGATCTACTTGTAAAAAATAATCAGGATCAGTTACTAGTGCMAAACCTGGATATCATGAT 2780
741 IleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGly 760
2781 ATCATCAAAATTCCACTGGAGCCACCAACATCGAAGTGAACAGCGGAACACAGAGGGA 2840
761 SerArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsn 780
2841 TCCAGGAACAATGSCACTTCTTTCCTCATCAAGCTCTGATGCGACATATATTCTTAAT 2900
781 GlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyValValLeuArg 800
2901 GGTGACTACACTTTGTCCACTTAGACCAAGACATTAATGACAAAGGTGTGTTCTTGAGG 2960
801 TyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeuLysGluPro 820
2961 TACAGCGGCTCTCTCGGGCATTTGGAAGAATTCGCAGCTTTAGCCCTCTCAAAAGAGCC 3020
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3021 TTGACCATCCAGGTTCTTACTGTGGGCAATGCCCTTCGACCTAAATTAATACACCTAC 3080
841 PheValLysLysLysLysGluSerPheAsnAlaIleProThrPheSerAlaTrpValIle 860
3081 TTCTAAAGAGAGAGAGAGATCTTTCATGCTATCCCACTTTTTCAGCATGGTCAAT 3140
861 GluGluTrpGlyGluCysSerLysSerCysGluLeuGlyTrpGlnArgArgLeuValGlu 880
3141 GAAGAGTGGGCGAATGTTCTAAGTCATGTGAATGGGTTGGCAGAGAAGACTGGTGAAG 3200
881 CysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLysProAlaSer 900
3201 TCCGAGACATTAATGACAGCTTCTCCAGTGTCCAGAGTCCAGAGTCCAGCCAGCCAGC 3260
901 ThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrpSerSerCys 920

QY 438 AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn 457
Db 1261 GACCACAGCCAGCGCTGGCTCTCTGCGAGTGCCTACATGATTACATCTTTGCGATAAT 1320
QY 458 GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu 477
Db 1321 GGTTCATGGGGAATGTTGATGGCAAGCTCAGAATCCCATCAGCTCCAGCGCATCTC 1380
QY 478 ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys 497
Db 1381 CTTGGCACCTGTGTACGATCCCAACCGGAGTGCAGTTTACATTTGGGGAGGACCTCCAAA 1440
QY 498 HisCysProAspAlaAsnThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly 517
Db 1441 CACTGCGCTGTATGACCCAGCACATGTAGCACTTGTGTGTACCGGCACTCTCTGTGGG 1500
QY 518 ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly 537
Db 1501 GTGCTGGTGTCTCAACCAACACACTCCCGTGGCGGATGGCAGCTGTGGAGAGGG 1560
QY 538 LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro 557
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QY 558 PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly 577
Db 1621 TTTTCATGGAGCTGGGGAATGTGGGGCTTGGGAGACTGTTCGAGAACGTGCGGTGA 1680
QY 578 GlyValGlnThrMetArgGlnCysAspAsnProValProLysAsnGlyGlyLysTyr 597
Db 1681 GGAGTCCAGTACACGATGAGGGAATGTGACAAACCCAGTCCCAAGAAATGGAGGGAATAC 1740
QY 598 CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsn 617
Db 1741 TGTGAAGGCAACGAGTGGCTGACAGATCTCTGTACCTTGAGGACTGTCCAGCAATAT 1800
QY 618 GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe 637
Db 1801 CGAAACCTTTAGAGAGGACAAATGTGAAGCACACACAGAGTTTCAAAACCTTCCTTT 1860
QY 638 GlySerGlyProAlaValGlnTrpIleProLysTyrAlaGlyValSerProLysAspArg 657
Db 1861 GGGAGTGGCGCTGCGGTGGAATGGATTCACCAAGTAGCTGGCTGTCCACCAAGGACAGG 1920
QY 658 CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal 677
Db 1921 TCCAAAGCTCATCTGCCAAGCCAAAGCAATGCTACTTCTGTTTTCAGGCCCAAGGT 1980
QY 678 ValAspGlyThrProCysSerProAspSerThrSerValCysValGlnCysVal 697
Db 1981 GTAGATGGTACTCCATGTAGCCCAAGATTCACCTCTGTCTGTGCAAGGACAGTGTGTA 2040
QY 698 LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys 717
Db 2041 AAAGCTGGTGTGTATGCGCATATAGACTCCAAAGAAAGAGTTTGAATGTGGTGTTC 2100
QY 718 GlyLysAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGly 737
Db 2101 GGGGGAATGATCTACTTGTAAAAAATATCAGGATCAGTACTAGTGCAAAACCTGGA 2160
QY 738 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 757
Db 2161 TATCATGATATCATCAATTCCTACTGGAGCCACCAATCGAAGTGAACAGCGGAAC 2220
QY 758 GlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAspGlyThrTyr 777
Db 2221 CAGAGGGGATCCAGGAACAATGGAGCTTTCTTGGCATCAAAAGCTGTGTGGCACATAT 2280
QY 778 IleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 797
Db 2281 ATTCTTAATGGTGACTACATCTTGTCCACCTTAGAGCAAGACATATGTACAAAGGTGT 2340

QY 798 ValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSerPheSerProLeu 817
Db 2341 GTCTTAGGTACAGCGGCTCTCTGCGCATTTGGAAGAAATTCGAGCTTTAGCCCTCTC 2400
QY 818 LysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArgProLysIleLys 837
Db 2401 AARGAGCCCTTGACCATCCAGGTTCCTTACTGTGGCAATGCCCTTCGACCTAAATTTAA 2460
QY 838 TyrThrTyrPheValLysLysLysGluSerPheAsnAlaIleProThrPheSerAla 857
Db 2461 TACACCTACTTCGTAAGAGAGAGAAATCTTTCAATGCTATCCCACTTTTTCAGCA 2520
QY 858 TrpValIleGluGluTrpGlyCysSerLysSerCysGluLeuGlyTrpGlnArgArg 877
Db 2521 TGGGTTCATGAGAGTGGGGCGAATGTTCTAAGTCATGTGAATGGGTGGCAGAGAAGA 2580
QY 878 LeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAlaLysGluValLys 897
Db 2581 CTGGTAGAATGCCGAGACATTAATGACAGCTGCTCCGAGTGTGCAAGAGAGTGAAG 2640
QY 898 ProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGlnLeuGlyGluTrp 917
Db 2641 CCAGCCAGCACACACCTTGTGCAGACCATCCCTGCCCCAGTGGCAGCTGGGGAGTGG 2700
QY 918 SerSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeuLysCysLeuSer 937
Db 2701 TCATCATGCTCTAAGACCTGTGGGAAGGTTTACAAAAAAGAGCTTGAAGTGTCTGTCC 2760
QY 938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
Db 2761 CATCATGGAGGGGTGTTATCTCATGAGAGCTGTGATCCTTTTAAAGAAACCTTAAACATTT 2820
QY 958 IleAspPheCysThrMetAlaGluCysSer 967
Db 2821 ATAGCTTTGCAACAATGGCAGAAATGCAGT 2850

RESULT 9
US-09-989-687-1
; Sequence 1, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2853)
; NAME/KEY: misc feature
; LOCATION: (3195)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3248)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3255)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (3261)
; OTHER INFORMATION: n is any nucleic acid
US-09-989-687-1

Alignment Scores:
Pred. No.: 0 Length: 3261
Score: 5144.00 Matches: 940

Percent Similarity:	99.37%	Conservative:	4
Best Local Similarity:	98.95%	Mismatches:	6
Query Match:	97.30%	Indels:	0
DB:	11	Gaps:	0
US-09-373-658c-126 (1-967) x US-09-989-687-1 (1-3261)			
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QY	38	LeuLeuAlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp	57
DB	61	CTGCTCCCGCGGGCTACTGGCGGTGTGGACGCACTCGGGCGCCCTCGAGGAGGAC	120
QY	58	GluGluLeuValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArg	77
DB	121	GAGGAGCTAGTGTGCGGAGCTGGAGCGGCCCGGACACCGGCTCCCGC	180
QY	78	LeuHisAlaPheAspGlnGlnLeuAspLeuAspValProAspSerSerPheLeuAla	97
DB	181	CTGCACGCTTTCACACAGCACTGGATCTGGAGCTGGGGCTCGGCGCCGACAGCATT	240
QY	98	ProGlyPheThrLeuGlnAsnValGlyArgGlySerGlySerAspThrProLeuProGlu	117
DB	241	CCCGGCTTCACGCTCCAGAACGTGGGGCGCAATCCGGGTCGAGACCGCCCTTCGCGAA	300
QY	118	ThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSerSerAlaAla	137
DB	301	ACCGACCTGGCGCACTGCTTCTACTCCGCGCACCGTGAATGGCGATCCAGCTCGGCTGCC	360
QY	138	AlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPhe	157
DB	361	GCCTCAGCTCTGCGAGGGCGGTGCGGGCGCCTTCTACTGCTGGGGAGCGATTTC	420
QY	158	IleGlnProLeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGluLysPro	177
DB	421	ATCCAGCGCTGCCCGCGCACGAGCGCTTGGCCACCGCCCGCCAGGGAGAGCCG	480
QY	178	ProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAspValGlyThr	197
DB	481	CCGGCACCACTCAGATTCCACCTCTCGGGCGGAAATCGGAGGGCGACGTAGCGGCAGC	540
QY	198	CysGlyValValAspAspGluProArgProThrGlyValAlaGluThrGluAspGluAsp	217
DB	541	TGGGGGTCTGTGACGACGAGCCCGCCCGCTCTGGGAGCGGAAATCGGAGGGCGAC	600
QY	218	GluGlyThrGluGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGln	237
DB	601	GAAGGGACTGAGGGCAGGACGAAGGCGCTCACTGGTCCCGCGCAGCACCGGCACTGCAA	660
QY	238	GlyValGlyGlnProThrGlyThrGlySerIleArgGlyLysArgPheValSerSerHis	257
DB	661	GGCGTAGGACAGCCCGCAGGACTGGAAGCATAGAAGAAAGCGATTGTGTCCAGTCAC	720
QY	258	ArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGly	277
DB	721	CGTATGTGGAACCATGCTTGTGGCAGACCACTCGATGCGCAGAAATTCACGGCAGTGT	780
QY	278	LeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSer	297
DB	781	CTAAGCATTTACCTTCTACGTTGTTCGGTGGCAGGATTTGTACAAACACCCCGCAGC	840
QY	298	IleArgAsnSerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLys	317
DB	841	ATTTCGTAAATCAGTTAGCTGTGGTGGTGAAGATCTTGGTCATCCACGATGACAGAG	900
QY	318	GlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCysAsnTrpGlnLys	337
DB	901	GGGCGGGAAGTCACTCCAAATGCTGCCCTCACTCTCGGAACTTTTGAACCTGGCAGAG	960
QY	338	GlnHisAsnProSerAspArgAspAlaGluHisTyrAspThrAlaIleLeuPheThr	357

DB	961	CAGCACAAACCCAGTCAGTCGGGATGACGACACTATGACACAGCAATTCCTTTCCACC	1020
QY	358	ArgGluAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThr	377
DB	1021	AGACAGACTTGTGTGGTCCCGACATGATGACTCTTGGGATGGCTGATGTGGAACT	1080
QY	378	ValCysAspProSerArgSerCysSerValIleGluAspGlyLeuGlnAlaAlaPhe	397
DB	1081	GTGTGTGATCCGAGCAGAGCTGCTCGTCATAGAAGATGATGTTTACAAGCTGCCTTC	1140
QY	398	ThrThrAlaHisGlnLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCys	417
DB	1141	ACCACAGCCCATGAATAGCCCACTGCTTTAAATGTCATGCCATGATGATGATGATGAT	1200
QY	418	AlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeu	437
DB	1201	GCACGCTTAATGTGTGAACCGAGATTCACATGATGGCTCAATGCTTTCCACCTG	1260
QY	438	AspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSerPheLeuAspAsn	457
DB	1261	GACCACAGCCAGCTTGGTCTCTCTGAGTGCCTACATGATTACATCATTTCTGGATAA	1320
QY	458	GlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeu	477
DB	1321	GGTCATGGGGAATGTTGATGGACAGCCCTCAGATCCCATACAGCTCCAGGCGATCTC	1380
QY	478	ProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLys	497
DB	1381	CTTGCCACCTCTGATGATGCCAACCGGCACTGCCAGTTCATATTTCGGGAGGACTCCAA	1440
QY	498	HisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGlyThrSerGlyGly	517
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QY	518	ValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGly	537
DB	1501	GTGCTGTGTGTCAACCAACCAACACTTCCGCTGGGCGGATGGCACCCAGCTGTGGAGGG	1560
QY	538	LysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAspThrPro	557
DB	1561	AAATGTGTATCAACGGCAAGTGTGTGAACAAACACGACAGAAAGCATTTTGTATACGCT	1620
QY	558	PheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArgThrCysGlyGly	577
DB	1621	TTTCATGGAGCTGGGGAATGTGGGGGCTTGGGAGACTGTTCAGAACACTGCGGTGGA	1680
QY	578	GlyValGlnTyrThrMetArgGluCysAspAsnProValProLysAsnGlyLysTyr	597
DB	1681	GGAGTCCAGTACAGATGAGGAAATGTGACAAACCCAGTCCCAAGAAATGGAGGAATAC	1740
QY	598	CysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCysProAspAsn	617
DB	1741	TGTGAAGGCAACGAGTGGCTTACAGATCTCTTAACCTTGGAGACTTCCACAGCAATAA	1800
QY	618	GlyLysThrPheArgGluGlnCysGluAlaHisAsnGluPheSerLysAlaSerPhe	637
DB	1801	GGAAAAACCTTTAGAGAGAACCAATGTGAAGCACACACAGAGTTTTTCAAGACTTCTTT	1860
QY	638	GlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSerProLysAspArg	657
DB	1861	GGGAGTGGGCTGCGGTGGAAATGCCATCCCAAGTACGCTGGCGCTCCACCAAGGACAG	1920
QY	658	CysLysLeuIleCysGlnAlaLysGlyIleGlyTyrPhePheValLeuGlnProLysVal	677
DB	1921	TGCAGCTCATCTGCCAAGCCAAAGCATTTGGCTACTTCTTCTTCTTTCAGGCCAAGTT	1980
QY	678	ValAspGlyThrProCysSerProAspSerThrSerValGlnGlyGlnCysVal	697
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QY	698	LysAlaGlyCysAspArgIleIleAspSerLysLysLysPheAspLysCysGlyValCys	717
DB	2041	AAAGCTGTTGTGATCGCATCATAGACTCCCAAAAGAAAGTTTGAATGTTGGTGTTC	2100

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QY 718 GlyGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSerAlaLysProGly 737
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QY 738 TyrHisAspIleIleThrIleProThrGlyAlaThrAsnIleGluValLysGlnArgAsn 757
DB 2161 TATCATGATATATCATCAATTCACCTCACTGAGGCCCAACATCGAAGTGAACAGGGGAC 2220
QY 758 GlnArgLysArgAsnAsnGlySerPheLeuAlaIleLysAlaAlaAspGlyThrTyr 777
DB 2221 CAGAGGGATCAGGAAACATGGCAGCTTCTTGCCATCAGAAGCTGCTGATGGACATAT 2280
QY 778 IleLeuAsnGlyAspTyrThrIleuSerThrLeuGluGlnAspIleMetTyrLysGlyVal 797
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DB 2701 TCATCATCTTCTTAAGACCTGTGGGAAGGGTTACAAAAAAGAAAGCTTGAAGTGTCTGTC 2760
QY 938 HisAspGlyGlyValLeuSerHisAspSerCysAspProLeuLysLysProLysHisPhe 957
DB 2761 CATGATGGAGGGGTGTTATCTCATGAGAGCTGTGATCTCTTAAAGAAACCTTAAACATTTT 2820
QY 958 IleAspPheCysThrMetAlaGluCysSer 967
DB 2821 ATAGACTTTTGCAATGGCAGAAATGCAGT 2850
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RESULT 10

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US-10-425-114-26851
; Sequence 26851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26851
; LENGTH: 4848
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4654-036-D4_FLI
US-10-425-114-26851
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Alignment Scores:
Pred. No.: 0 Length: 4848
Score: 5140.50 Matches: 956
Percent Similarity: 92.40% Conservative: 4
Best Local Similarity: 92.01% Mismatches: 7
Query Match: 97.23% Indels: 73
DB: 13 Gaps: 1
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US-09-373-658C-126 (1-967) x US-10-425-114-26851 (1-4848)

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QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 502 GCGAGCGGGCTCCCGGGTCTCGGAGCTTTGGGCCGCTACCCACGCTGCTGCTGCC 561
QY 41 AlaAlaLeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAspGluLeu 60
DB 562 GCGCGCTACTGCGCGTGTCCGACGCTCCGGCGCCCTCCGAGGAGGAGGAGGAGCTA 621
QY 61 ValValProGluLeuGluArgValProGlyHisGlyThrThrArgLeuArgLeuHisAla 80
DB 622 GTGTGCGCGAGCTGGAGCGGCCCGGGACACGGGACCGCGCTCCGCTGCACGCC 681
QY 81 PheAspGlnGlnLeuAspLeuAspValProPheAspSerSerPheLeuAlaProGlyPhe 100
DB 682 TTTACACGAGCTGGAATCTGGAGCTCCGCCCGACAGAGCTTTTGGCGCGCGGCTTC 741
QY 101 ThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeuProGluThrAspLeu 120
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QY 121 AlaHisCysPheThrSerGlyThrValAsnGlyAspProSerSerAlaAlaLeuSer 140
DB 802 GCGCACTGCTTACTCCGCGACCTGGAATGGCGATCCAGCTCGGCTCGCGCTCAGC 861
QY 141 LeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnPro 160
DB 862 CTCTGCGAGGGCTGCGCGCGCTTCTACTCTGCGGAGGCGGTATTTATCTCAGCCG 921
QY 161 LeuProAlaAlaSerGluArgLeuAlaThrAlaAlaProGlyGlyLysProAlaPro 180
DB 922 CTGCGCGCGCGAGCGGCTCGCCACCGCGCCCGAGGAGGAGGAGGAGGAGGAGGAG 981
QY 181 LeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyValGlyGlyThrCysGlyVal 200
DB 982 CTACAGTTCCACTCTCTGCGCGAATCGGCGGCGAGCTAGGCGGCGAGCTGCGGGTG 1041
QY 201 ValAspAspGluProArgProThrGlyLysAlaGluThrGluAspGluAspGluGlyThr 220
DB 1042 GTGGACGAGCGCGCGCGCTGGGAAAGCGAGCGAGCGAGCGAGCGAGCGAGCGACT 1101
QY 221 GluGlyGluAspGluGlyProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGly 240
DB 1102 GAGGGCGAGGAGGAGGCTCAGTGTGTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1161
QY 241 GlnProThrGlyThrGlySerIleArgLysLysArgPheValSerSerHisArgTyrVal 260
DB 1162 CAGCCACAGGAACTGGAGGAGCATAGAAGAGAGCGATTGTGTCAGTACCGCTATGTG 1221
QY 261 GluThrMetLeuValAlaAspGlnSerMetAlaGluPheHisGlySerGlyLeuLysHis 280
DB 1222 GAAACCATCTTGTGGCAGACCATGATGCGAGATTCACGGGAGTGGTCTTAAAGCAT 1281
QY 281 TyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyrLysHisProSerIleArgAsn 300
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Db 1282 TACCTTCTCAGCTGTGTTTTCGGTGGCAGCCAGGATGTACAAACACCCAGCATTCGTAAT 1341
Qy 301 SerValSerLeuValValValLysIleLeuValIleHisAspGluGlnLysGlyProGlu 320
Db 1342 TCAGTTTASCTGTGGTGGTGAAGATCTTGCTCATCCACGATGAACAGAGGGCGCGAA 1401
Qy 321 ValThrSerAsnAlaLaLeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsn 340
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Qy 361 LeuCysGlySerGlnThrCysAspThrLeuGlyMetAlaAspValGlyThrValCysAsp 380
Db 1522 TTGTGTGGGTCCAGACATGTGATCTTGGGATGGCTGATTTGGAACTGTGTGTGAT 1581
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Db 1582 CCGAGCAGAAAGCTGCTCCGTATAGAGATGATGTTTACAGCTGCTTCCACACAGCC 1641
Qy 401 HisGluLeuGlyHisValPheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeu 420
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Qy 421 AsnGlyValAsnGlnAspSerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSer 440
Db 1702 AATGGTGTGAACAGGATTCACACATGATGGCTCATGCTTCCAACTCCAGCCACAGC 1761
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Db 1762 CAGCCTTGTGCTCTTTCGAGTGGCTACATGATPACATCATTTTCTGGATTAATGTCATGG 1821
Qy 461 GluCysLeuMetAspLysProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThr 480
Db 1822 GATGTTTGTAGACCAAGCTCAGATCCATA-CAGCTCCAGCGCATCTCCCTGGCACC 1880
Qy 481 SerTyrAspAlaAsnArgGlnCysGlnPheThrPheGlyGluAspSerLysHisCysPro 500
Db 1881 TGTAGATGCCAACCGGAGTGCAGTTTACATTTGGGGAGGACTCCAAACACTGCCCT 1940
Qy 501 AspAlaAspSerThrCysSerThrIleuTrpCysThrGlyThrSerGlyValLeuVal 520
Db 1941 GATGCAGCCAGCACATGTATGACCTTGTGGTGTACCGGACCTCTGGTGGGTGTGGTG 2000
Qy 521 CysGlnThrLysHisPheProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCys 540
Db 2001 TGTCAAACCAACACTTCCCGTGGCGGATGGCACCAGCTGTGGAGAGGGAAATGGTGT 2060
Qy 541 IleAsnGlyLysCysValAsnLysAsnHisArgLysHisPheAsp 555
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Db 2121 GAACACATTCAGATTGAAAGAAACAAGTGTGTAAAGATATGATACCAAGTTAAA 2180
Qy 555 ----- 555
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Qy 555 ----- 555
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Qy 556 ----- ThrProPheHisGlySerTrpGlyMetTrpGlyProTrpG1 569
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Qy 569 YAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCysAspAsnPr 589
Db 2361 AGACTGTTGGAGAACGTGGCGTGGAGGATCCAGTACATGATGAGGGAATGTGACAAACC 2420

Qy 589 oValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSerCysAs 609
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Qy 609 nLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHi 629
Db 2481 CCTTGGAGACTGTCCAGACATTAATGGAATAACCTTTAGAGAGAAACAATGTGAAGACA 2540
Qy 629 sAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTy 649
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Qy 769 aIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGl 789
Db 2961 CATCAAGCTGCTGATGACACATATATCTTAATGTCGACTACACTTTTGTCCACCTTGA 3020
Qy 789 uGlnAspIleMetTyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGl 809
Db 3021 GCAAGACATTTATGACAAAGGTGTGTCTTGAGGTACACGGCTCTCTCGCGGCATGGA 3080
Qy 809 uArgIleArgSerPheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGl 829
Db 3081 AAGAATTCGAGCTTTAGCCCTCTCAAGAGCCCTTGACCATCCAGGTTCCTTACTGTGG 3140
Qy 829 yAsnAlaLeuArgProLysIleLysTyrThrTyrPheValLysLysLysLysGluSerPh 849
Db 3141 CAATGCCCTTCGACCTAAATTAATAACCTACTTCTGTAAGAAGAAAGAAAGGAATCTTT 3200
Qy 849 eAsnAlaIleProThrPheSerAlaTtpValIleGluGluTrpGlyCysSerLysSe 869
Db 3201 CAATGCTATCCCACTTTTTCAGCATGGTCTATTGAAGATGGGGCGAATGTTCTAAGTC 3260
Qy 869 rCysGluLeuGlyTrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAl 889
Db 3261 ATGTGAATTGGGTGGCAGAGACACTGGTGAATGCCAGACATTAATGACAGCCTGC 3320
Qy 889 aSerGluCysAlaLysGluValLysProAlaSerThrArgProCysAlaAspHisProCy 909
Db 3321 TTCGAGTGTCCAAAGGAAGTGAAGCCAGCACCAAGACCTTGTGAGACCATCCCTCG 3380
Qy 909 sProGlnTrpGlnLeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyL 929
Db 3381 CCCCCAGTGGCAGCTGGGGAGTGTGTATCATGTTCTTAAGACCTGTGGGAAGGTACAA 3440
Qy 929 sLysThrSerLeuLysCysLeuSerHisAsnGlyGlyValLeuSerHisAspSerCysAs 949
Db 3441 AAAAAGAGCTTGAAGTGTGTGCTCCCATGATGGAGGGGTGTATCTCATGAGAGCTGTGA 3500

QY 949 pProLeuLysLysProLysHisPhePheIleAspPheCysThrMetAlaGluCysSer 967
DB 3501 TCCCTTTAAGAAACCTTAAACATTTTCATAGACTTTTGCACAATGGCAGATGCAGT 3555

RESULT 11
US-10-152-319A-1840
; Sequence 1840, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1840
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_024400
US-10-152-319A-1840

Alignment Scores:
Pred. No.: 0 Length: 4878
Score: 4287.00 Matches: 790
Percent Similarity: 87.17% Conservative: 59
Best Local Similarity: 81.11% Mismatches: 111
Query Match: 81.09% Indels: 14
DB: 12 Gaps: 5

US-09-373-658C-126 (1-967) x US-10-152-319A-1840 (1-4878)

QY 1 MetGlnArgAlaValProGluGlyPheGlyArgGlyLysLeuGlySerAspMetGlyAsn 20
DB 395 ATGCAGCCAGAAAGTCCCTTTGGGGTCCAGGCAAGCTGAAGCCCTCTCAGACATGGGGGAC 454

QY 21 AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuAla 40
DB 455 ATCCAGCGGGCAGCGAGATTTCGAGAGTCTCAGTCTTCGACACATGCTGTGTACTCTCCTC 514

QY 41 AlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSerGluGluAsp 57
DB 515 GCTTCCATCAACAAAGTCTGTGTGTGGGGCGGCACACGGGGCGCCCGGAGGAGAC 574

QY 58 GluGluLeuValValProGluLeuGluArgValProGlyHis-----GlyThrArgLeu 76

DB 575 GAGGAGCTGGTGTGCTCCCTCGCTGGAGCGCCCGCGGGCCACGATTCACACACATCCTC 634
QY 77 ArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspValProProAspSerSerPheLeu 96
DB 635 CGTCTGGAGCGCTTGTGTGTCAGCAGCTGCATCTGAAGTTGACAGCAGACAGCGGTTCCTTA 694
QY 97 AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu--- 115
DB 695 GCGCTTGGCTTCACTCCCTCCAGACGGTGGGGCGAGTCTCTGGTCCGAGCAGCAGCATCTG 754
QY 116 ---ProGluThrAspLeuAlaHisCysPheThrSerGlyThrValAsnGlyAspProSer 134
DB 755 GACCCCACTGGGAGCTGGCCACTGCTTCTACTCTGGACCGGTGAACGGTGAACCCGACG 814
QY 135 SerAlaAlaLeuSerLeuCysGlyValArgGlyAlaPheGlyLeuGlyGlu 154
DB 815 TCGCGCGCGCCCTCAGCCTGTGAAGGTGTGCGCGTGTCTTCTACCTACCTACCAAGGGGAG 874
QY 155 AlaThrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThrAlaAlaPro 173
DB 875 GAGTCTTCAATTCAGCCAGCGCTTGGTGGCCACCGAGCGCTTGTCCCGCCGCAACCG 934
QY 174 GlyLysProProAlaProLeuGlnPheHisLeuLeuArgAsnArgGlnGlyAsp 193
DB 935 AAGGAGGAGTCAATCGCACCTCCGCGGTTCACATCTCAGGCGGAGCGCGGGGCGGAGC 994
QY 194 ValGlyGlyThrCysGlyValValAspAspGluProArgProThrGlyLysAlaGluThr 213
DB 995 GCGCGCGCAAAAGTGGGTGTGTCAGGAGGAGAGACCCCTGCGCAACC----- 1039
QY 214 GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAsp 233
DB 1040 -----AGCACTCGGTTCGCGAAGCCAGAACACACCCCGACCGCTCTCTCGGAGAC 1093
QY 234 ProAlaLeuGlnGlyValGlyGlnProThrGlyThrGlySerIleArgLysLysArgPhe 253
DB 1094 CCCACTCTCAGGGCGCGGAAAGCCACAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
QY 254 ValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe 273
DB 1154 GTGTCCAGCCCCGTTATGTGGAAACCATGCTCTGTGGTGGCTGACCGTCCATGGTGTGCTTC 1213
QY 274 HisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyr 293
DB 1214 CAGCGCAGCGCTCTAAAGCATTAACCTTCTTAACCTTCTCGGTGGCAGCAGCATTTTAC 1273
QY 294 LysHisProSerIleArgAsnSerValSerLeuValValValLysIleLeuValIleHis 313
DB 1274 AAGCACCAGCATTAGGAATTCATATGCTGTGGTGGTGAAGATCTTTGGTGCATATAT 1333
QY 314 AspGluGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys 333
DB 1334 GAGGAGCAGAGGAGCAGGAGGAGTACTTCCAATGCGCTCTCACCTTAGGAATTTCTGT 1393
QY 334 AsnTrpGlnLysGlnHisAsnProProSerAspArgAspAlaGluHisTyrAspThrAla 353
DB 1394 AGCTGCGAGAAACAGCACACACAGCCCGAGTCCGAGATCCAGAGCAGCATATGACAGCG 1453
QY 354 IleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAla 373
DB 1454 ATTCGTCTCACCAGACAGGATTTATGTGGTCCCAACCTGTGACACTCTCGGATGGCT 1513
QY 374 AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu 393
DB 1514 GATGTTGGAACTGTATGTGACCCCGAGAGAGTGTTCGGTTCATCGAAGATGATGTTT 1573
QY 394 GlnAlaAlaPheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp 413
DB 1574 CAGGCTGCTTCCACACAGCCCATGATTTGGGCACTGTGTTTAACTGACACACAGCATGAC 1633
QY 414 AlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetLaserMet 433

Db 1634 GCCAAGCACTGCCGCGAGCTTTAATGGCGGTGAGTGGGGATTCCCATCTGATGGCCCTCGATG 1693
Qy 434 LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyTyrMetIleThrSer 453
Db 1694 CTCTCCAGCTTGGACACAGCAGCCCTCGTCTCTCTTCGAGTGCTCATCATGCTGCACATCA 1753
Qy 454 PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu 473
Db 1754 TTCTGGCAACCGCCATGGGGAATGTTTATGGACCAAGCGCAGAACCCCAATCAAGCTC 1813
Qy 474 ProGlyAspLeuProGlyThrSerTyrAspAlaAsnArgGlnCysGlnPheThrPheGly 493
Db 1814 CCAATCTGATCTTCCCGGTACTCTTACGATGTCACCAACCGCCAGTGTCACTTACCTTCGGG 1873
Qy 494 GluAspSerLysHisCysProAspAlaSerThrCysSerThrLeuTrpCysThrGly 513
Db 1874 GAGAAATCCACGCACTCCCTCGATGCGCCAGCAGCATGCACTCCCTGTGTGTCACCTGGC 1933
Qy 514 ThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyThrSer 533
Db 1934 ACCTCCGGTGGCTTACTGGTGTGCCAACAACAACACTTCCCTTGGGCGATGGACCCAGC 1993
Qy 534 CysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHis 553
Db 1994 TGGCGAAGAGGGAATGGTGTGCAGCGGCAAGTGTGTGAACAAGACCGACATGAAGCAC 2053
Qy 554 PheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArg 573
Db 2054 TTTGCTACTCTCTTCAATGGAGCTGGGACCGTGGGACCATGGGAGACTGCTCAAGA 2113
Qy 574 ThrCysGlyGlyGlyValGlnTrpMetArgGluCysAspAsnProValProLysAsn 593
Db 2114 ACCTGTGTGGAGAGTTCAATATACATGAGAGAATGTGACAACCGGTGCCAAGAAGAC 2173
Qy 594 GlyGlyLysTrpCysGluGlyLysArgValArgTyrArgSerCysAsnLeuGluAspCys 613
Db 2174 GGGGGAGAGTACTGCCAAGGCAAAACGAGTCCGCTACAGSTCCCTGTAAACATTGAGGACTGT 2233
Qy 614 ProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSer 633
Db 2234 CCAGACAATAACGGAAACATTCAGAGAGAGCAATGGAGCGGCAACATGATGTTTCC 2293
Qy 634 LysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysTyrAlaGlyValSer 653
Db 2294 AAAGCTTCCTTTGGGAATGAACCCAGCGTGGATGGACACCCCAAGTATGTGGCGTCTCG 2353
Qy 654 ProLysAspArgCysLysLeuLysGlnAlaLysGlyIleGlyTyrPhePheValLeu 673
Db 2354 CCNAGACAGGTGCAAGCTTACCTCGAAGCCCAAGGCAATGGCTACTTCTTTGTTTA 2413
Qy 674 GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln 693
Db 2414 CAGCCCAAGTGTAGATGGCACTCCCTGTAGTCCAGACTTACTTCTGTGTGTGCAA 2473
Qy 694 GlyGlnCysValLysAlaGlyCysAspArgIleLeuAspSerLysLysLysPheAspLys 713
Db 2474 GGCAGTGTGTAAGACTGCTGTGATCATCATAGACTCCAAAAGAAAGTTCGATAG 2533
Qy 714 CysGlyValCysGlyGlyAsnGlySerThrCysLysLysLysLysLysLysLysLysLys 733
Db 2534 TGTGGCGTTTGTGGAGAAATGGCTCCAGTGCACAGAAATATCAGAACGTCCTACTAGT 2593
Qy 734 AlaLysProGlyTyrHisAspIleIleThrProThrGlyAlaThrAsnIleGluVal 753
Db 2594 ACAAGACCTGGGTATCATGACATTTGCACAAATTCCTGTGGAGCCCAACCAATGAAGTG 2653
Qy 754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaIa 773
Db 2654 AAACATCGTAATCCAGAGGGGATCCAGAAACATAGGCGAGTTTCTGGCTATTAGAGCTGCA 2713
Qy 774 ArgGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793
Db 2714 GATGGTACCTATATTCTGAATGGAACCTTCACTCTGTCCACTCTAGAGCAAGACCTCACC 2773

Qy 794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813
Db 2774 TACAAAGGTACTGTCCTTAAAGATACATGAGTCTCTCAGACGATTCGAAAGAACCCGAGC 2833
Qy 814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833
Db 2834 TTTAGTCCACTCAAGAACCCCTGACCATCCAGGTTCTTATGGTGGGCCATGCTCTCCGA 2893
Qy 834 ProLysIleLysTyrThrTyrPheValLysLysLysLysLysLysLysLysLysLysLys 853
Db 2894 CCCAAATCACTACACCTATTTATGAAGAAGACACGAGCCCTTCAACGCTATTCCC 2953
Qy 854 ThrPheSerAlaTrpValIleGluGluTrpGlyGluCysSerLysSerCysGluLeuGly 873
Db 2954 ACATTTTCCGAGTGGGTGATTGAAGAGTGGGGGAGTGTCCCAAGACATGTGTTCCGGT 3013
Qy 874 TrpGlnArgArgLeuValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893
Db 3014 TGCAGAGAGAGTGGTAGAGTGCAGAGACATTAATGACACCCCTCTTCTGAATGTGCC 3073
Qy 894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913
Db 3074 AAAGAAGTCAAGCCAGCCAGTACACGACCTTGTGCAGACCTTCTTGCACACGTTGCCAG 3133
Qy 914 LeuGlyGluTrpSerSerCysSerLysThrCysGlyLysGlyTyrLysThrSerLeu 933
Db 3134 GTGGGGATTTGTCACTTCTTAAACTTGTGGAGAGGGTTATAAGAGAGAACCTTGT 3193
Qy 934 LysCysLeuSerHisAspGlyValLeuSerHisAspSerCysAspProLeuLysLys 953
Db 3194 AAATGTCTGCCATGATGGCGTGTGTATATCAATGAGAGCTGTGATCTTTGAAGAAA 3253
Qy 954 ProLysHisPheIleAspPheCysThrMetAlaGluCysSer 967
Db 3254 CCNAGCAATTACATTGACTTTTGCATACTACACACAGTCAGT 3295

RESULT 12
US-10-191-803-170
; Sequence 170, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-50900S
; CURRENT APPLICATION NUMBER: US/10/191,803
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 170
; LENGTH: 4878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_024400
US-10-191-803-170

Alignment Scores:
Pred. No.: 0 Length: 4878
Score: 4287.00 Matches: 790

Percent Similarity:	87.17%	Conservative:	59
Best Local Similarity:	81.11%	Mismatches:	111
Query Match:	81.09%	Indels:	14
DB:	16	Gaps:	5

US-09-373-658C-126 (1-367) x US-10-191-803-170 (1-4878)

QY	1	MetGlnArgAlaValProGluGlyPheGlyArgArgLysLeuGlySerAspMetGlyAsn	20
Db	395	ATGACCCAGAAAGTCCCTTTGGGGTTCAGCAAGCTTGAAGCCCTGCTCAGACATCGGGGAC	454
QY	21	AlaGluArgAlaProGlySerArgSerPheGlyProValProThrLeuLeuLeuLeuAla	40
Db	455	ATCCAGCGGCGACGAGTTTCGGAGCTCTCMGTCTGCACACATGCTGTGTGCTACTCTCT	514
QY	41	AlaAla-----LeuLeuAlaValSerAspAlaLeuGlyArgProSerSerGluGluAsp	57
Db	515	GCTTCCATTAACAATGCTGTGTGTGTCGGGCGCACACGGGCGCCCCACCGAGGAAGAC	574
QY	58	GluGluLeuValValProGluLeuGluArgValProGlyHis---GlyThrThrArgLeu	76
Db	575	GAGGAGCTGGTCTGCCCTTCGCTGAGCGCGCCCGGGCGCACAGATTCACACACACTCTCT	634
QY	77	ArgLeuHisAlaPheAspGlnLeuLeuAspValProProAspSerSerPheLeu	96
Db	635	CGTCTGGACGCCCTTTGGTCAGCAGCTGCATCTGGAAGTTGCAGCCAGACACGGGTTCCTTA	694
QY	97	AlaProGlyPheThrLeuGlnAsnValGlyArgLysSerGlySerAspThrProLeu---	115
Db	695	GGCGCTGGCTTCACCCCTCCACGCGTGGGGCGCGAGTCTCGGTCCGAGGCACACATCTG	754
QY	116	---ProGluThrAspLeuAlaHisCysPheTyrSerGlyThrValAsnGlyAspProSer	134
Db	755	GACCCCACTGGGGACCTGGCCCACTGCTTCTACTCTGGCACGCTGAACGCTGACCCACG	814
QY	135	SerAlaAlaLeuSerLeuCysGluGlyValArgGlyAlaPheTyrLeuLeuGlyGlu	154
Db	815	TCCGGCGCGCGCTCAGCCTCTGTGAAGGTGTGGCGGTGCTTCTACCTTACACAGCGAG	874
QY	155	AlaTyrPheIleGlnProLeuProAla---AlaSerGluArgLeuAlaThrAlaAlaPro	173
Db	875	GAGTCTCTCATTCAGCCAGCGCTTCGGTGGCCACCAGCGCTGTGTCCTCCCGCCGAACCG	934
QY	174	GlyGluLysProProAlaProLeuGlnPheHisLeuLeuArgArgAsnArgGlnGlyAsp	193
Db	935	AAGGAGGAGTCAATCGCACCTCCCGCGTTCACATCTCGAGCGAAGGCGGGCGGGCAGC	994
QY	194	ValGlyGlyThrCysGlyValValAspGluProArgProThrGlyLysAlaGluThr	213
Db	995	GCGCGCCGAAGTGGGTGTGTCATGGAGAGAGACCTCTGCCAACCC-----	1053
QY	214	GluAspGluAspGluGlyThrGluGlyGluAspGluGlyProGlnTrpSerProGlnAsp	233
Db	1040	-----AGCAACTCGGGTTCGCAAGACGAGAACACCCCGGACCGTGGCTCTCGCGAAC	1099
QY	234	ProAlaLeuGlnGlyValGlyGlnProThrClyThrGlySerIleArgLysIleArgPhe	253
Db	1094	CCCCTCTCAGGCGCGGGAAGCCCAACAGGACCGAGGAAGCAATAGGAAGAGCGATTT	1153
QY	254	ValSerSerHisArgTyrValGluThrMetLeuValAlaAspGlnSerMetAlaGluPhe	273
Db	1154	GTGTCCAGCCCGCTTATGTGGAACACCATGCTCTGTGCTGACCACTCCATGCTGCATTC	1213
QY	274	HisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSerValAlaAlaArgLeuTyr	293
Db	1214	CACGGCAGCGGTCTAAGACATTAACCTTCTAACCTTCTTCGGTGGCAGCCAGATTTTAC	1273
QY	294	LysHisProSerIleArgAsnSerValSerLeuValValLysIleLeuValIleHis	313
Db	1274	AAGCACCCAGCATTAAGAAATTCATAGTCTGGTGGTGGAGATCTTGGTCAATAT	1333
QY	314	AspGlnGlnLysGlyProGluValThrSerAsnAlaAlaLeuThrLeuArgAsnPheCys	333

1334	Db	GAGGAGCAGAGGGACCGGAAGTTACTTTCCAAATGCGCGCTCTCAACCTTTAGGAATTTCTGT	1393
334	QY	AsnTrpGlnLysGlnHisAsnProSerAspArgAspAlaGluHisItyrAspThrAla	353
1394	Db	AGCTGGCAGAAACAGCAACAACAGCCCGAGTGACCGGGATCCAGAGCACTATGACACAGCG	1453
354	QY	IleLeuPheThrArgGlnAspLeuCysGlySerGlnThrCysAspThrLeuGlyMetAla	373
1454	Db	ATTCTTGTTTCCACAGACAGGATTTATGTGGCTCCACACCTGTGTGACACTCTCGGATGGCT	1513
374	QY	AspValGlyThrValCysAspProSerArgSerCysSerValIleGluAspAspGlyLeu	393
1514	Db	GATGTTGGAACTGTATGTAGCCCAACGACGAGAGCTGTTCCGTCATCGAAGATGATGGTTTA	1573
394	QY	GlnAlaIlePheThrThrAlaHisGluLeuGlyHisValPheAsnMetProHisAspAsp	413
1574	Db	CAGGCTGCTCTTCCACACAGCCCATGAAATGGGGCATGTGTTTAACTATGCCACACAGATGAC	1633
414	QY	AlaItyrGlnCysAlaSerLeuAsnGlyValAsnGlnAspSerHisMetMetAlaSerMet	433
1634	Db	GCCAAAGCACTGCCGACGTTTAAATGGGGTGAGTGGGGATTTCCCATCTCATGTGGCTCGATG	1693
434	QY	LeuSerAsnLeuAspHisSerGlnProTrpSerProCysSerGlyItyrMetIleThrSer	453
1694	Db	CTCTCCACTTGGACCAACAGCCAGCCCTGGTCTCTTTCGAGTGCTCATATGGTGCACATCA	1753
454	QY	PheLeuAspAsnGlyHisGlyGluCysLeuMetAspLysProGlnAsnProIleGlnLeu	473
1754	Db	TTCTTGGACACAGCCCATGGGGAATGTTTATGTGACAGCCGACAGAACCCAAATCAGCTC	1813
474	QY	ProGlyAspLeuProGlyThrSerItyrAspAlaAsnArgGlnCysGlnPheThrPheGly	493
1814	Db	CCATCTGATCTTCCCGGTACCTTGACGATGCCAAACCGCCAGTGTCAAGTTTACCTTCGGG	1873
494	QY	GluAspSerLysHisCysProAspAlaAlaSerThrCysSerThrLeuTrpCysThrGly	513
1874	Db	GAGGAATCCAGCGACTGCCCTGATGACGACGACACATGCAAGTACCTGTGTGCATCGGC	1933
514	QY	ThrSerGlyGlyValLeuValCysGlnThrLysHisPheProTrpAlaAspGlyItyrSer	533
1934	Db	ACCTCCGGTGGCTTACTGGTGTGCCAAACAAACACTTCCCTTGGGCAGATGSCACAGC	1993
534	QY	CysGlyGluGlyLysTrpCysIleAsnGlyLysCysValAsnLysAsnHisArgLysHis	553
1994	Db	TGCGGAGAGGGAAATGGTGTGTGCGGGCAAGTGTGTAAACAAAGACCCGACATGAAGCAC	2053
554	QY	PheAspThrProPheHisGlySerTrpGlyMetTrpGlyProTrpGlyAspCysSerArg	573
2054	Db	TTTGCTACTCTGTTCATGGAGACTGGGACCGTGGGGACCATGGGGAGACTGCTCAAGA	2113
574	QY	ThrCysGlyGlyGlyValGlnItyrThrMetArgGluCysAspAsnProValProLysAsn	593
2114	Db	ACCTGTGGTGGAGAGTTCAATATACAATGAGAGAATGTGACAAACCCGGTCCCAAGAAC	2173
594	QY	GlyGlyLysItyrCysGluGlyLysArgValArgItyrArgSerCysAsnLeuGluAspCys	613
2174	Db	GGGGGGAAGTACTGCCAGGACCAACGAGTCCGCTACAGTCTCTGTAAACATGTGAGACTGT	2233
614	QY	ProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGluAlaHisAsnGluPheSer	633
2234	Db	CCAGACAATAACGGAAAAACATTCAGAGAGGAGCAATGCCGCGCACCAATCAGTTTTCC	2293
634	QY	LysAlaSerPheGlySerGlyProAlaValGluTrpIleProLysItyrAlaGlyValSer	653
2294	Db	AAGAGCTTCTTTTGGGAATGAACCCAGCGGGAATGGACACCCCAAGTATGCTGGCGTCTCG	2353
654	QY	ProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIleGlyItyrPhePheValLeu	673
2354	Db	CCAAAGGACAGGTGCAGCTTACTCGCGAAGCCAAAGGCAATGGCTACTCTTCTGTGTTTA	2413
674	QY	GlnProLysValValAspGlyThrProCysSerProAspSerThrSerValCysValGln	693
2414	Db	CAGCCCAAGGTGATGGCACTCCCTGACTCCAGACTTACTTCTGTCTGTGTGCA	2473

QY 694 GlyGlnCysValLysAlaGlyCysAspArgIleAlaSerLysLysLysPheAspLys 713
Db 2474 GGACAGTGTGTGAAGCTGCTGTGATCGCATCATAGACTCCAAAAGAGTTCGATAAG 2533
QY 714 CysGlyValCysGlyCysGlyAsnGlySerThrCysLysLysLysSerGlySerValThrSer 733
Db 2534 TGTGGGGTTTGTGGAGGAATGCTCCAGTGCAGAGAAATATCAGAACGGTCACTAGT 2593
QY 734 AlaLysProGlyThrHisAspIleIleThrProThrGlyAlaThrAsnIleGluVal 753
Db 2594 ACAAGACCTGGGTATCATGACATTGTGCACAAATTCCTGGTGGAGCCCAACATGAGTG 2653
QY 754 LysGlnArgAsnGlnArgGlySerArgAsnAsnGlySerPheLeuAlaIleLysAlaAla 773
Db 2654 AAACATCGTAAATCCAGGGAGTCCAAACATATGGCAGCTTCTGGCTATTAGAGCTGA 2713
QY 774 AspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSerThrLeuGluGlnAspIleMet 793
Db 2714 GATGTGACCTATATTCTGAATGAAACTTCACCTGTCTGCTCCACTAGAGCAAGCTCACC 2773
QY 794 TyrLysGlyValValLeuArgTyrSerGlySerSerAlaAlaLeuGluArgIleArgSer 813
Db 2774 TCAAAAGGTACTGTCTTAAGATACAGTGTTCCTCAGCAGCATTTGGAAGAAATCCGCAGC 2833
QY 814 PheSerProLeuLysGluProLeuThrIleGlnValLeuThrValGlyAsnAlaLeuArg 833
Db 2834 TTATGTCCTCAAGAACCCCTGACCATCCAGTTCCTATGTTGGGCCATGCTCTCCGA 2893
QY 834 ProLysIleLysTyrThrTyrPheValLysLysLysGlySerPheAsnAlaIlePro 853
Db 2894 CCCAAATCAAGTACACCTATTTTATGAAGAAGAGACGAGCCCTTCAACGCTATTCC 2953
QY 854 ThrPheSerAlaTyrValIleGluGluTyrGlyCysSerLysSerCysGluLeuGly 873
Db 2954 ACATTTTCGAGTGGGTGATTGAAGAGTGGGGAGTGTCTCAAGACATGTGTTCCGGT 3013
QY 874 TrpGlnArgGluValGluCysArgAspIleAsnGlyGlnProAlaSerGluCysAla 893
Db 3014 TGGCAGAGGAGAGTGTGTAGATGCAGAGACATTAATGAGACACCTTCTTCTGAATGTGC 3073
QY 894 LysGluValLysProAlaSerThrArgProCysAlaAspHisProCysProGlnTrpGln 913
Db 3074 AAAGAAGTGAAGCCAGCCAGTACCAGACCTGTGGCAGACCTTCTTGTCCCACTGTGGCAG 3133
QY 914 LeuGlyGluTrpSerCysSerLysThrCysGlyLysGlyTyrLysLysThrSerLeu 933
Db 3134 GTGGGGGATTGTTACCATGTTCTAAACTGTGGGAGGGTTATTAAGAGAGACCTTG 3193
QY 934 LysCysLeuSerHisAspGlyValLeuSerHisAspSerCysAspProLeuLysLys 953
Db 3194 AAATGTCTCTCCATGATGGCGTGTGTATCAATGAGAGCTGTGATCCTTTGAAGAA 3253
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Db 3254 CCAAGACATTACATTGACTTTTGCATCTACACACAGTGTGAGT 3295

RESULT 13

US-09-373-658-20
Sequence 20, Application US/09373658
Publication No. US20030092900A1
GENERAL INFORMATION:
APPLICANT: Iruela-Arispe, Luisa
APPLICANT: Hastings, Gregg A.
APPLICANT: Ruben, Steven M.
APPLICANT: Jonak, Zdenka L.
APPLICANT: Trulli, Stephen H.
APPLICANT: Fronwald, James A.
APPLICANT: Terrett, Jonathan A.
TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
FILE REFERENCE: 1488.1070006
CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 20
LENGTH: 4180
TYPE: DNA
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-373-658-20

Alignment Scores:
Pred. No.: 0 Length: 4180
Score: 4277.50 Matches: 789
Percent Similarity: 86.65% Conservative: 61
Best Local Similarity: 80.43% Mismatches: 110
Query Match: 80.91% Indels: 21
DB: 10 Gaps: 6

US-09-373-658C-126 (1-967) x US-09-373-658-20 (1-4180)

QY 1 MetGlnArgAlaValPro-----GlulysPheGlyArgArgLysLeu 14
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QY 15 GlySerAspMetGlyAsnAlaGluArgAlaProGlySerArgSerPheGlyProValPro 34
Db 432 TCTCTCGACATGGGGGACGTCCAGCGGCGCAGAGATCTCGGGGCTCTCTGTCGCCACAC 491
QY 35 ThrLeuLeuLeuAlaAla-----LeuLeuAlaValSerAspAlaLeuGly 51
Db 492 ATGCTGTTGCT 551
QY 52 ArgProSerGluGluAspGluLeuValProGluLeuGluArgValProGlyHis 71
Db 552 CGCCCGCAGGAGAGATGAGAGCTGTCTGCTGAGCGCTTTGGCCAGCAGCTACATCTGAAGTTG 671
QY 72 Gly-----ThrArgLeuArgLeuHisAlaPheAspGlnGlnLeuAspLeuAspVal 89
Db 612 GATTCACACACACACACGCTTCTGCTGAGCGCTTTGGCCAGCAGCTACATCTGAAGTTG 671
QY 90 ProProAspSerSerPheLeuAlaProGlyPheThrLeuGlnAsnValGlyArgLysSer 109
Db 672 CAGCGGACACGGTTTCTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
QY 110 GlySerAspThrProLeu-----ProGluThrAspLeuAlaHisCysPheTyrSerGly 127
Db 732 GGGTCCGAGGCACACACACCTGAGCCCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
QY 128 ThrValAsnGlyAspProSerSerAlaAlaLeuSerLeuCysGluGlyValArgGly 147
Db 792 ACGGTGAACGGTGTATCCCGGCTGCGCGAGCGCTTCTGAGAGGCTGTGAGAGGCTGTGAGAGG 851
QY 148 AlaPheTyrLeuLeuGlyGluAlaTyrPheIleGlnProLeuPro-----AlaAlaSerGlu 166
Db 852 GCCTTCTACCTACAGGAGAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 911
QY 167 ArgLeuAlaThrAlaAlaProGlyGluLysProAlaProLeuGlnPheHisLeuLeu 186
Db 912 CGCTTGGCCCTCGCGTGGCGAGAGAGTCTTCTGCGAGCGCGCTGCGAGCGCGCTGCGAGCGCG 971
QY 187 ArgArgAsnArgGlnGlyAspValGlyThrCysGlyValValAspAspGluProArg 206
Db 972 AGCGAGGCGCGGGGCGAGTGGCGGCGCGAGTGGCGGCGCGCTGCGAGCGAGCGAGCGAGCGCG 1031
QY 207 ProThrGlyLysAlaGluThrGluAspGluAspGluGlyThrGluGluAspGluGly 226
Db 1032 CCAACC-----AGCGACTCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 1070
QY 227 ProGlnTrpSerProGlnAspProAlaLeuGlnGlyValGlnGlnProThrGlyThrGly 246
Db 1071 AACCATGTGCTGCGGGACCCCGCTCAGGACGCGGGAAAGCAATCAGGACAGGACAGGACAGG 1130
QY 247 SerIleArgLysLysArgPheValSerSerHisArgTyrValGluThrMetLeuValAla 266

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Db 1191 GACCAAGTCCATGCGCGACTTCCAGCGCAGCGCTTAAGACATTAACCTTCAACCTGTTC 1250
Qy 287 SerValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 306
Db 1251 TCGGTGGCAGCGAGGTTTACAGCATCCACCATTAAGCAATTAAGTCCGCTGTGGTG 1310
Qy 307 ValLysIleLeuValIleHisAspGluGlnLysGlyProGluValThrSerAsnAlaAla 326
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Qy 327 LeuThrLeuArgAsnPheCysAsnTrpGlnLysGlnHisAsnProProSerAspArgAsp 346
Db 1371 CTCACCCCTTCGGAATTTCTGCAAGCTGGCAGAAACACACACACGCGCGAGTACCGGAT 1430
Qy 347 AlaGluHisTyrAspThrAlaIleLeuPheThrArgGlnAspLeuCysGlySerGlnThr 366
Db 1431 CCAGAGCACTATGACACCTGCAATTCGTTTACACAGCAGGATTTATGTGGCTCCACACG 1490
Qy 367 CysAspThrLeuGlyMetAlaAspValGlyThrValCysAspProSerArgSerCysSer 386
Db 1491 TGTGACACTCTCGGAATGCGCATGTTGGAACCGTATGTGTACCCAGCAGGAGCTGTCTCA 1550
Qy 387 ValIleGluAspAsnGlyLeuGlnAlaAlaPheThrAlaHisGluLeuGlyHisVal 406
Db 1551 GTCATAGAGATGATGGTTTGAACCGCTTTCACACAGCCCATGAATTTGGCCCATGTG 1610
Qy 407 PheAsnMetProHisAspAspAlaLysGlnCysAlaSerLeuAsnGlyValAsnGlnAsp 426
Db 1611 TTTAACATGCGCCAGCATGATCTAAGCACTGTGCGCAGCTTGAATGGTGTGAGTGGCGAT 1670
Qy 427 SerHisMetMetAlaSerMetLeuSerAsnLeuAspHisSerGlnProTrpSerProCys 446
Db 1671 TCTCATCTGCGCTCGCATGCTCTCCAGCTTAGACCATGACGACCCCTGTCTCACTTTC 1730
Qy 447 SerGlyTyrMetIleThrSerPheLeuAspAsnGlyHisGlyGluCysLeuMetAspLys 466
Db 1731 AGTGCTACATGGTCACGCTCTCTCTAGATAATGAGACAGCGGGAATGTTTGTATGGACAG 1790
Qy 467 ProGlnAsnProIleGlnLeuProGlyAspLeuProGlyThrSerTyrAspAlaAsnArg 486
Db 1791 CCCCAGAAATCCAATCAAGCTCCCTCTGATCTTCCCGGTACCTTGTACGATGCCAACCGC 1850
Qy 487 GlnCysGlnPheThrPheGlyGluAspSerLysHisCysProAspAlaAlaSerThrCys 506
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Qy 507 SerThrLeuTyrCysThrGlyThrSerGlyGlyValLeuValCysGlnThrLysHisPhe 526
Db 1911 ACTACCTGTGTGTCACCTGGCACCTCCGCTGCTTACTGGTGTGCTGCTGCTGCTGCTG 1970
Qy 527 ProTrpAlaAspGlyThrSerCysGlyGluGlyLysTrpCysIleAsnGlyLysCysVal 546
Db 1971 CTTGGGAGATGGCCAGCTGTGAGAGGAGGAGTGTGTGTGTCAGTGGCAAGTGGCGTG 2030
Qy 547 AsnLysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGly 566
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Qy 567 ProTrpGlyAspCysSerArgThrCysGlyGlyValGlnTyrThrMetArgGluCys 586
Db 2091 CCGTGGGAGAGCTGCTCAAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2150
Qy 587 AspAsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArg 606
Db 2151 GACAAACCCAGTCCCAAGAACCGAGGAGTACTGTGAGGAGGAGGAGGAGGAGGAGGAGG 2210
Qy 607 SerCysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGlnCys 626

Db 2211 TCTGTGAACATCTCGAGGACTGTCTCAGACAATAACGGAATAACGTTTCAGAGAGCAGTGC 2270
Qy 627 GluAlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTyrIle 646
Db 2271 GAGCGGCACATAGTATTCTTCAAAGCTTCTTTGGGAATGAGCCCACTGTAGATGGACA 2330
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Db 2331 CCCAAGTACGCGCGCTCTGCCAAAGGACAGGTCGAAGCTCACCTGTGAAGCCAAAGGC 2390
Qy 667 IleGlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAsp 686
Db 2391 ATTGGCTACTTTTTCGTTCTACACCCCAAGGTTGTAGTGCACCTCCCTGTAGTCCAG 2450
Qy 687 SerThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleLeuAsp 706
Db 2451 TCTACCTCTGTCTGTGCAAGGCGAGTGTGGAAGCTGGCTGTGATCGCATCATAGAC 2510
Qy 707 SerLysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLys 726
Db 2511 TCCAAAGAAGATTTGATTAAGTGTGGGTTTGTGAGGAAACGGTTCACATGCAAGAG 2570
Qy 727 IleSerGlySerValThrSerAlaLysProGlyTyrHisAspIleIleThrIleProThr 746
Db 2571 ATGTACGGAATAGTCACTAGTACAAAGCACTGGGTATCATGACATGTGCACAAATCTCT 2630
Qy 747 GlyAlaThrAsnIleGluValLysGlnArgAsnGlnArgGlySerArgAsnAsnGlySer 766
Db 2631 GGAGCCACCACATTTGAAGTGAACATCGGAATCAAAGGGGTCCAGAAACATGGCAGC 2690
Qy 767 PheLeuAlaIleLysAlaAlaAspGlyThrTyrIleLeuAsnGlyAspTyrThrLeuSer 786
Db 2691 TTTCTGCTATTAGAGCGCTGATGTACCTATATTTCTGAATGGAACCTTCACTCTGTCC 2750
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Qy 847 GluSerPheAsnAlaIleProThrPheSerAlaTrpValIleGluGluTyrGlyGluCys 866
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Qy 967 Ser 967
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862	Db	TGGCGGATGGCACCAAGCTGGGAGAGGAAATCGTGATCAACGCGCAAGTGTGTGAAC	921
548	QY	LysAsnHisArgLysHisPheAspThrProPheHisGlySerTrpGlyMetTrpGlyPro	567
922	Db	AAAACCCAGCAGGAGCAATTTTGATACGCCCTTTTCATGGAGCTGGGACCACATGGGGACCG	981
568	QY	TrpGlyAspCysSerArgThrCysGlyGlyGlyValGlnTyrThrMetArgGluCysAsp	587
982	Db	TGGGGAGACTGTTTCGAGAAACCTCGCGTGGAGGAGTCCAGTACACGATGAGGGCAATGTGAC	1041
588	QY	AsnProValProLysAsnGlyGlyLysTyrCysGluGlyLysArgValArgTyrArgSer	607
1042	Db	AAACCCAGTCCAAAGAAATCGAGGGAGACTCTGTGAGGCCAAACGAGTGCCTACAGATCC	1101
608	QY	CysAsnLeuGluAspCysProAspAsnAsnGlyLysThrPheArgGluGluGlnCysGlu	627
1102	Db	TGTAACTTGAGGACTGTCCAGACAATAATGGAAAAACCTTTAGAGAGGAAACAATGTGAA	1161
628	QY	AlaHisAsnGluPheSerLysAlaSerPheGlySerGlyProAlaValGluTrpIlePro	647
1162	Db	GCACACAACGAGTTTCAAAGCTTCCTTTGGCAGTGGGCCCTCGCGTGGAAATGGATCCC	1221
648	QY	LysTyrAlaGlyValSerProLysAspArgCysLysLeuIleCysGlnAlaLysGlyIle	667
1222	Db	AGTAGCTTGGCGTCTCCAAAGGACAGGTGCAAGCTCATCTGCCAAGCCAAAGGCATT	1281
668	QY	GlyTyrPhePheValLeuGlnProLysValValAspGlyThrProCysSerProAspSer	687
1282	Db	GGCTACTTCTTCGTTTGGAGCCCAAGTTGTTGATGGTACTCCATGTAGCCCGAGATCC	1341
688	QY	ThrSerValCysValGlnGlyGlnCysValLysAlaGlyCysAspArgIleIleAspSer	707
1342	Db	ACCTCTGTCTGTGTCCAGGACAGTGTGTAAAGCTGGTTGTGATCGCATCATGACTCC	1401
708	QY	LysLysLysPheAspLysCysGlyValCysGlyGlyAsnGlySerThrCysLysLysIle	727

Search completed: June 18, 2004, 23:46:31
Job time : 1081.83 secs

Mon Jun 21 11:43:52 2004

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Page 23

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RESULT 14
US-09-989-687-20
; Sequence 20, Application US/09989687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 4180
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-989-687-20

Alignment Scores:
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Score: 4277.50
Length: 4180
Percent Similarity: 86.65%
Matches: 789
Best Local Similarity: 80.43%
Conservative: 61
Mismatch: 110
Query Match: 80.91%
Indels: 21
Gaps: 6
DS: 11
US-09-373-658C-126 (1-967) x US-09-989-687-20 (1-4180)

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Db 3111 CTTCTCTTGGCCACACTGGCAGGTGGGGGATGGTCAACCATGTTCACAAACTTGGCGGAG 3170

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (1) .. (2184)
US-09-445-023A-2

Alignment Scores:
Pred. No.: 0 3922.00 2184
Score: 3922.00 707
Percent Similarity: 98.89%
Best Local Similarity: 98.19%
Query Match: 74.18%
DB: 9 0 0

US-09-373-558C-126 (1-967) x US-09-445-023A-2 (1-2184)

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Qy 268 GlnSerMetAlaGluPheHisGlySerGlyLeuLysHisTyrLeuLeuThrLeuPheSer 287
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Qy 288 ValAlaAlaArgLeuTyrLysHisProSerIleArgAsnSerValSerLeuValVal 307
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Qy 308 LysIleLeuValIleHisAspGluGlnIyGlyProGluValThrSerAsnAlaAlaLeu 327
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Qy 328 ThrLeuArgAsnPheCysAsnTyrGlnLysGlnHisAsnProProSerAspArgAla 347
Db 262 ACTCTGCGGAACCTTTTGCACACTGGCAGAGCAGCACAAACCCAGTACCGGGGATGCA 321